STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number 143453

TO: Patricia Duffy **Location: REM/3B05/3C18** **Art Unit: 1645** **Thursday, March 31, 2005** **Case Serial Number: 10/033243**	**From: Barb O'Bryen** **Location: Biotech-Chem Library** **Remsen 1a69** **Phone: 571-272-2518** **barbara.obryen@uspto.gov**

Search Notes

STIC-Biotech/ChemLib 148453

From: Duffy, Patricia
Sent: Tuesday, March 22, 2005 10:21 AM
To: STIC-Biotech/ChemLib
Subject: Sequence search 10/033,243

In re: 10/033,243

Please search SEQ ID NO:132.
Please include both a commercial and interference database hit.

Note: this is a short NA, and I a print out of all 100% hits.

Thanks,

Patricia A. Duffy, Ph.D.
Art Unit 1645
Remsen 3B05; Mailbox 3C18
571-272-0855

****
STAFF USE ONLY

Searcher:_____
Searcher Phone: 2-
Date Searcher Picked up:____
Date Completed:_____
Searcher Prep/Rev. Time:___
Online Time:_____

****
Type of Search

NA#:_____ AA#:_____
Interference:____ SPDI:___
S/L:_____ Oligomer:_____
Encode/Transl:_____
Structure#:_____ Text:___
Inventor:____ Litigation:___

****
Vendors and cost where applicable
STN:_____
DIALOG:_____
QUESTEL/ORBIT:_____
LEXIS/NEXIS:_____
SEQUENCE SYSTEM:_____
WWW/Internet:_____
Other(Specify):_____

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 30, 2005, 10:48:12 ; Search time 1811 Seconds
(without alignments)
561.877 Million cell updates/sec

Title: US-10-033-243-132
Perfect score: 21
Sequence: 1 tcgtcgaacgttcgagatgat 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	21	100.0	21	6	AX592442	AX592442 Sequence
2	19	90.5	19	6	AX592329	AX592329 Sequence
3	19	90.5	22	6	AX592340	AX592340 Sequence
4	18.4	87.6	110000	1	AE016822_01	Continuation (2 of
5	18	85.7	19	6	AX592334	AX592334 Sequence
6	17.8	84.8	164921	8	AF022186	AF022186 Cyanidium
7	17.4	82.9	19	6	AX592366	AX592366 Sequence
8	17.4	82.9	19	6	AX592367	AX592367 Sequence
9	17	81.0	19	6	AX592333	AX592333 Sequence
c 10	16.8	80.0	198	8	BAS540263	AJ540263 Unculture
11	16.8	80.0	658	3	TRE512595	AJ512595 Timarcha
c 12	16.8	80.0	3041	3	AF257638	AF257638 Drosophil
c 13	16.8	80.0	3047	3	AF257637	AF257637 Drosophil
c 14	16.8	80.0	3047	3	AF257639	AF257639 Drosophil
c 15	16.8	80.0	3047	3	AF257640	AF257640 Drosophil
c 16	16.8	80.0	3047	3	AF257641	AF257641 Drosophil
c 17	16.8	80.0	3047	3	AF257643	AF257643 Drosophil
c 18	16.8	80.0	3047	3	AF257646	AF257646 Drosophil
c 19	16.8	80.0	3050	3	AF257642	AF257642 Drosophil
c 20	16.8	80.0	3050	3	AF257644	AF257644 Drosophil
c 21	16.8	80.0	3050	3	AF257645	AF257645 Drosophil
c 22	16.8	80.0	3050	3	AF257647	AF257647 Drosophil
c 23	16.8	80.0	3050	3	AF257648	AF257648 Drosophil
c 24	16.8	80.0	3050	3	AF257649	AF257649 Drosophil
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26	16.8	80.0	193764	2	CR450831	CR450831 Danio rer
27	16.4	78.1	18	6	AX592324	AX592324 Sequence
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c 29	16.4	78.1	23	6	AR352575	AR352575 Sequence
c 30	16.4	78.1	23	6	AX083677	AX083677 Sequence
c 31	16.4	78.1	23	6	AX148638	AX148638 Sequence
c 32	16.4	78.1	23	6	AX250703	AX250703 Sequence
c 33	16.4	78.1	23	6	AX252293	AX252293 Sequence
c 34	16.4	78.1	23	6	AX252511	AX252511 Sequence
c 35	16.4	78.1	23	6	AX252522	AX252522 Sequence
c 36	16.4	78.1	23	6	AX252936	AX252936 Sequence
c 37	16.4	78.1	23	6	AX253115	AX253115 Sequence
c 38	16.4	78.1	23	6	AX253125	AX253125 Sequence
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c 45	16.2	77.1	2064	5	AF069993	AF069993 Gallus ga

ALIGNMENTS

RESULT 1
AX592442
LOCUS AX592442 21 bp DNA linear PAT 27-JAN-2003
DEFINITION Sequence 132 from Patent WO02052002.
ACCESSION AX592442
VERSION AX592442.1 GI:27950544
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Fearon,K.L. and Dina,D.
TITLE Immunomodulatory polynucleotides and methods of using the same
JOURNAL Patent: WO 02052002-A 132 04-JUL-2002;
Dynavax Technologies Corporation (US)
FEATURES Location/Qualifiers
source 1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
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/note="Polynucleotide containing CG"
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.59;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGAACGTTCGAGATGAT 21
||||||||||||||||||||
Db 1 TCGTCGAACGTTCGAGATGAT 21

RESULT 2
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LOCUS AX592329 19 bp DNA linear PAT 27-JAN-2003
DEFINITION Sequence 19 from Patent WO02052002.
ACCESSION AX592329
VERSION AX592329.1 GI:27950431
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

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REFERENCE   1
  AUTHORS   Fearon,K.L. and Dina,D.
  TITLE     Immunomodulatory polynucleotides and methods of using the same
  JOURNAL   Patent: WO 02052002-A 19 04-JUL-2002;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
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ORIGIN

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Db          1 TCGTCGAACGTTCGAGATG 19


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LOCUS       AX592340                 22 bp    DNA     linear   PAT 27-JAN-2003
DEFINITION  Sequence 30 from Patent WO02052002.
ACCESSION   AX592340
VERSION     AX592340.1  GI:27950442
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Fearon,K.L. and Dina,D.
  TITLE     Immunomodulatory polynucleotides and methods of using the same
  JOURNAL   Patent: WO 02052002-A 30 04-JUL-2002;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
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ORIGIN

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Db          4 TCGTCGAACGTTCGAGATG 22


RESULT 4
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WPCOMMENT
  Sequence split into 26 fragments  LOCUS AE016822 Accession AE016822
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     AE016822_01       100001    210000
     AE016822_02       200001    310000
     AE016822_03       300001    410000
     AE016822_04       400001    510000
     AE016822_05       500001    610000
     AE016822_06       600001    710000
     AE016822_07       700001    810000
     AE016822_08       800001    910000
     AE016822_09       900001   1010000
     AE016822_10      1000001   1110000
     AE016822_11      1100001   1210000
     AE016822_12      1200001   1310000
     AE016822_13      1300001   1410000
     AE016822_14      1400001   1510000
     AE016822_15      1500001   1610000
     AE016822_16      1600001   1710000
     AE016822_17      1700001   1810000
     AE016822_18      1800001   1910000
     AE016822_19      1900001   2010000
     AE016822_20      2000001   2110000
     AE016822_21      2100001   2210000
     AE016822_22      2200001   2310000
     AE016822_23      2300001   2410000
     AE016822_24      2400001   2510000
     AE016822_25      2500001   2584158
Continuation (2 of 26) of AE016822 from base 100001 (AE016822 Leifsonia xyli subsp. xyli

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RESULT 5
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LOCUS       AX592334                 19 bp    DNA     linear   PAT 27-JAN-2003
DEFINITION  Sequence 24 from Patent WO02052002.
ACCESSION   AX592334
VERSION     AX592334.1  GI:27950436
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Fearon,K.L. and Dina,D.
  TITLE     Immunomodulatory polynucleotides and methods of using the same
  JOURNAL   Patent: WO 02052002-A 24 04-JUL-2002;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
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ORIGIN

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  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATG 19
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Db          1 TCGTNGAACGTTCGAGATG 19


RESULT 6
AF022186
LOCUS       AF022186              164921 bp    DNA     circular PLN 14-DEC-2000
DEFINITION  Cyanidium caldarium strain RK1 chloroplast, complete genome.
ACCESSION   AF022186 Z36235 Z70297
VERSION     AF022186.2  GI:6466296
KEYWORDS    .
SOURCE      chloroplast Cyanidium caldarium
  ORGANISM  Cyanidium caldarium
            Eukaryota; Rhodophyta; Bangiophyceae; Cyanidiales; Cyanidiaceae;
            Cyanidium.
REFERENCE   1  (bases 130696 to 132364)
  AUTHORS   Vogel,H., Fischer,S. and Valentin,K.
  TITLE     A model for the evolution of the plastid sec apparatus inferred
            from secY gene phylogeny
  JOURNAL   Plant Mol. Biol. 32 (4), 685-692 (1996)
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  MEDLINE   97134960
   PUBMED   8980520
REFERENCE   2  (bases 1 to 164921)
  AUTHORS   Glockner,G., Rosenthal,A. and Valentin,K.
  TITLE     The structure and gene repertoire of an ancient red algal plastid
            genome
  JOURNAL   J. Mol. Evol. 51 (4), 382-390 (2000)
  MEDLINE   20496959
   PUBMED   11040290
REFERENCE   3  (bases 46857 to 47851)
  AUTHORS   Valentin,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-MAR-1996) Institute for Plant Physiology, Justus
            Liebig University, Heinrich Buff Ring 58-62, Giessen 35392, Germany
REFERENCE   4  (bases 28701 to 75580)
  AUTHORS   Gloeckner,G., Rosenthal,A. and Valentin,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-SEP-1997) Department of Genome Analysis, IMB Jena,
            Beutenbergstr.11, Jena 07745, Germany
REFERENCE   5  (bases 1 to 164921)
  AUTHORS   Gloeckner,G., Rosenthal,A. and Valentin,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-NOV-1999) Genome Analysis, Institute for Molecular
            Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany
REFERENCE   6  (bases 130696 to 132364)
  AUTHORS   Vogel,H., Fischer,S. and Valentin,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-NOV-1999) Institute for Plant Physiology, Justus
            Liebig University, Heinrich Buff Ring 58-62, Giessen 35392, Germany
COMMENT     On or before Nov 23, 1999 this sequence version replaced gi:529651,
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                     /db_xref="taxon:2771"
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     stem_loop       339. .477
                     /note="stem-loop separates direct repeat unit"
     rep_origin      580. .780
                     /note="similiar to yeast mitochondrial origin of
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                     RGGKIGLFGGAGVGKTVLIMELINNVAKAHGGVSVFGGVGERTREGNDLYQEMKESGV
                     INEKDLNLSKVALCYGQMNEPPGARMRVGLTALTMAEYFRDVNKQNVLLFIDNIFRFV
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  Best Local Similarity   90.5%;  Pred. No. 1.3e+02;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATGAT 21
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RESULT 7
AX592366
LOCUS       AX592366                  19 bp    DNA     linear   PAT 27-JAN-2003
DEFINITION  Sequence 56 from Patent WO02052002.
ACCESSION   AX592366
VERSION     AX592366.1  GI:27950468
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Fearon,K.L. and Dina,D.
  TITLE     Immunomodulatory polynucleotides and methods of using the same
  JOURNAL   Patent: WO 02052002-A 56 04-JUL-2002;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
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ORIGIN

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  Best Local Similarity   94.7%;  Pred. No. 75;
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Qy          1 TCGTCGAACGTTCGAGATG 19
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Db          1 TCGTCGGACGTTCGAGATG 19


RESULT 8
AX592367
LOCUS       AX592367                  19 bp    DNA     linear   PAT 27-JAN-2003
DEFINITION  Sequence 57 from Patent WO02052002.
ACCESSION   AX592367
VERSION     AX592367.1  GI:27950469
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Fearon,K.L. and Dina,D.
  TITLE     Immunomodulatory polynucleotides and methods of using the same
  JOURNAL   Patent: WO 02052002-A 57 04-JUL-2002;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Polynucleotide containing CG"
ORIGIN

  Query Match             82.9%;  Score 17.4;  DB 6;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 75;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATG 19
              |||||| ||||||||||||
Db          1 TCGTCGTACGTTCGAGATG 19


RESULT 9
AX592333
LOCUS       AX592333                  19 bp    DNA     linear   PAT 27-JAN-2003
DEFINITION  Sequence 23 from Patent WO02052002.
ACCESSION   AX592333
VERSION     AX592333.1  GI:27950435
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Fearon,K.L. and Dina,D.
  TITLE     Immunomodulatory polynucleotides and methods of using the same
  JOURNAL   Patent: WO 02052002-A 23 04-JUL-2002;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
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                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Polynucleotide containing CG"
     misc_feature    2
                     /note="n = 5-bromocytocine"
     misc_feature    5
                     /note="n = 5-bromocytocine"
ORIGIN

  Query Match             81.0%;  Score 17;  DB 6;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 1.3e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATG 19
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Db          1 TNGTNGAACGTTCGAGATG 19


RESULT 10
BAS540263/c
LOCUS       BAS540263               198 bp    DNA     linear   PLN 09-SEP-2004
DEFINITION  Uncultured basidiomycete partial lac gene for laccase, exons 1-2,
            clone S6-H3-Seq5.
ACCESSION   AJ540263
VERSION     AJ540263.1  GI:41367247
KEYWORDS    lac gene; laccase.
SOURCE      uncultured basidiomycete
  ORGANISM  uncultured basidiomycete
            Eukaryota; Fungi; Basidiomycota; environmental samples.
REFERENCE   1
  AUTHORS   Luis,P., Walther,G., Kellner,H., Martin,F. and Buscot,F.
  TITLE     Diversity of laccase genes from basidiomycetes in a forest soil
  JOURNAL   Soil Biol. Biochem. 36, 1025-1036 (2004)
REFERENCE   2  (bases 1 to 198)
  AUTHORS   Luis,P.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-JAN-2003) Luis P., Institute of Ecology,
            Friedrich-Schiller-University Jena, Dornburger Str. 159, 07743
            Jena, GERMANY
FEATURES             Location/Qualifiers
     source          1. .198
                     /organism="uncultured basidiomycete"
                     /mol_type="genomic DNA"
                     /isolation_source="brown forest soil"
                     /db_xref="taxon:175244"
                     /clone="S6-H3-Seq5"
                     /country="Germany:Bavaria, Steigerwald"
     gene            1. .198
                     /gene="lac"
     mRNA            join(<1. .120,177. .>198)
                     /gene="lac"
     CDS             join(<1. .120,177. .>198)
                     /gene="lac"
                     /EC_number="1.10.3.2"
                     /function="phenoloxidase"
                     /codon_start=1
                     /product="laccase"
                     /protein_id="CAD62526.1"
                     /db_xref="GI:41367248"
                     /db_xref="UniProt/TrEMBL:Q70UJ9"
                     /translation="HWHGFFQKHTNYDDGPSFVTQCPIIPNESFTYDFSVPDQAGTFW
                     YHS"
     exon            <1. .120
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                     /number=1
     intron          121. .176
                     /gene="lac"
                     /number=1
     exon            177. .>198
                     /gene="lac"
                     /number=2
ORIGIN

  Query Match             80.0%;  Score 16.8;  DB 8;  Length 198;
  Best Local Similarity   90.0%;  Pred. No. 2.2e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATGA 20
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Db        154 TCGTCGACCGTTCGACATGA 135


RESULT 11
TRE512595
LOCUS       TRE512595               658 bp    DNA     linear   INV 18-AUG-2003
DEFINITION  Timarcha recticollis 5.8S rRNA gene (partial), 28S rRNA (partial)
            and ITS2, isolate 160.
ACCESSION   AJ512595
VERSION     AJ512595.1  GI:33945511
KEYWORDS    28S ribosomal RNA; 28S rRNA gene; 5.8S ribosomal RNA; 5.8S rRNA
            gene; internal transcribed spacer 2; ITS2.
SOURCE      Timarcha recticollis
  ORGANISM  Timarcha recticollis
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
            Phytophaga; Chrysomeloidea; Chrysomelidae; Chrysomelinae;
            Timarchini; Timarcha.
REFERENCE   1
  AUTHORS   Gomez-Zurita,J. and Vogler,A.P.
  TITLE     Incongruent nuclear and mitochondrial phylogeographic patterns in
            the Timarcha goettingensis species complex (Coleoptera,
            Chrysomelidae)
  JOURNAL   J. Evol. Biol. 16, 833-843 (2003)
REFERENCE   2  (bases 1 to 658)
  AUTHORS   Gomez-Zurita,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-OCT-2002) Gomez-Zurita J., Department of Entomology,
            The Natural History Museum, Cromwell Road, London SW7 5BD, UNITED
            KINGDOM
FEATURES             Location/Qualifiers
     source          1. .658
                     /organism="Timarcha recticollis"
                     /mol_type="genomic DNA"
                     /isolate="16"
                     /db_xref="taxon:79533"
                     /country="Spain:Pla de l'Artiga, Lleida"
     gene            1. .79
                     /gene="5.8S rRNA"
     rRNA            <1. .79
                     /gene="5.8S rRNA"
                     /product="5.8S ribosomal RNA"
     misc_feature    80. .622
                     /note="internal transcribed spacer 2, ITS2"
     gene            623. .658
                     /gene="28S rRNA"
     rRNA            623. .>658
                     /gene="28S rRNA"
                     /product="28S ribosomal RNA"
ORIGIN

  Query Match             80.0%;  Score 16.8;  DB 3;  Length 658;
  Best Local Similarity   90.0%;  Pred. No. 2.6e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 CGTCGAACGTTCGAGATGAT 21
              || |||||||||| |||||
Db        228 CGGCGAACGTTCGAAATGAT 247


RESULT 12
AF257638/c
LOCUS       AF257638               3041 bp    DNA     linear   INV 09-OCT-2000
DEFINITION  Drosophila simulans strain CT96_2s hexokinase-t1 and hexokinase-t2
            genes, complete cds.
ACCESSION   AF257638
VERSION     AF257638.1  GI:10765243
KEYWORDS    .
SOURCE      Drosophila simulans
  ORGANISM  Drosophila simulans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 3041)
  AUTHORS   Duvernell,D.D. and Eanes,W.F.
  TITLE     Contrasting molecular population genetics of four hexokinases in
            Drosophila melanogaster and Drosophila simulans
  JOURNAL   Genetics (2000) In press
REFERENCE   2  (bases 1 to 3041)
  AUTHORS   Duvernell,D.D. and Eanes,W.F.
  TITLE     Direct Submission
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  JOURNAL   Submitted (19-APR-2000) Ecology and Evolution, State University of
            New York, Stony Brook, NY 11794, USA
FEATURES             Location/Qualifiers
     source          1. .3041
                     /organism="Drosophila simulans"
                     /mol_type="genomic DNA"
                     /strain="CT96_2s"
                     /db_xref="taxon:7240"
     mRNA            <1. .>1398
                     /product="hexokinase-t1"
     CDS             1. .1398
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                     /protein_id="AAG22945.1"
                     /db_xref="GI:10765244"
                     /translation="MANTFNPEEDFPEVYKVCKLFNPSIDDLEKIKQAMDREITMGLS
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                     IMPHTVAAGRGTEVFTFLATIIANFVKEKKVDKDNLPLGIAFAFTLKKLALDVGILVS
                     WTKEFGAQGAIGKDVVQLLRDALAKFPEISVDVMGIINVGAGSLLALCWAQPDTRIGL
                     IMGSIANSCYVERVERCETYEGDEFRRLMIINSDWAHFGDTGQLDFIRNEFDRLLDTD
                     SINPGTRIYEKFSGALCMGELVRIIVLRLMKAGAIFAEDRRDYIGIQWKLDMVSLIEI
                     VSDPPGVYTKAQEVMDKFRIRHCKERDLAALKYICDTVTNRAAMLVASGVSCLIDRMR
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                     ANKYKTDAKLFTMDY"
     mRNA            join(<1609. .2118,2190. .>3041)
                     /product="hexokinase-t2"
     CDS             join(1609. .2118,2190. .3041)
                     /codon_start=1
                     /product="hexokinase-t2"
                     /protein_id="AAG22946.1"
                     /db_xref="GI:10765245"
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                     RAVIKCFVSHVQDLPTGKERGKYLALDLGGSNFRVLLVNLISNSDVEIMSKGYNFPLT
                     LMSGSGKALFDFLAESLSEFCHTHGLENESLPLGFTFSFPLQQQGLSKGILVAWTKGF
                     SCEGVVGKNVVSLLQEAIDRRGDIKINTVAILNDTVGTLMSCAFYHPNCRIGLIVGTG
                     SNACYVEKTVNAECFEGYQTSPKPSMIINCEWGAFGDNGVLEFVRTSYDKIVDKVTPN
                     PGKQTFEKCISGMYMGELVRLVVIDMIAKGFMFHGIISEKIQERWSFKTAYISDVESD
                     APGEYRNCNKVLSELGILGCQEPDKEALRYICEAVSSRSAKLCACGLVTIINKMNINE
                     VVIGIDGSVYRFHPKYHDMLQYHMKKLLKPGVKFELIVSEDGSGRGAALVAATAVQAK
                     SKL"
ORIGIN

  Query Match             80.0%;  Score 16.8;  DB 3;  Length 3041;
  Best Local Similarity   90.0%;  Pred. No. 3.1e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 CGTCGAACGTTCGAGATGAT 21
              |||||||||  |||  ||||||
Db        156 CGTCGAACGATCGTGATGAT 137


RESULT 13
AF257637/c
LOCUS       AF257637               3047 bp    DNA     linear   INV 09-OCT-2000
DEFINITION  Drosophila simulans strain DPF96_3s hexokinase-t1 and hexokinase-t2
            genes, complete cds.
ACCESSION   AF257637
VERSION     AF257637.1  GI:10765240
KEYWORDS    .
SOURCE      Drosophila simulans
  ORGANISM  Drosophila simulans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 3047)
  AUTHORS   Duvernell,D.D. and Eanes,W.F.
  TITLE     Contrasting molecular population genetics of four hexokinases in
            Drosophila melanogaster and Drosophila simulans
  JOURNAL   Genetics (2000) In press
REFERENCE   2  (bases 1 to 3047)
  AUTHORS   Duvernell,D.D. and Eanes,W.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-APR-2000) Ecology and Evolution, State University of
            New York, Stony Brook, NY 11794, USA
FEATURES             Location/Qualifiers
     source          1. .3047
                     /organism="Drosophila simulans"
                     /mol_type="genomic DNA"
                     /strain="DPF96_3s"
                     /db_xref="taxon:7240"
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                     /product="hexokinase-t1"
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                     IMPHTVAAGRGTEVFTFLATIIANFVKEKKVDKDNLPLGIAFAFTLKKLALDVGILVS
                     WTKEFGAQGAIGKDVVQLLRDALAKFPEISVDVMGIINVGAGSLLALCWAQPDTRIGL
                     IMGSIANSCYVERVERCETYEGDEFRRLMIINSDWAHFGDTGQLDFIRNEFDRLLDTD
                     SINPGTRIYEKFSGALCMGELVRIIVLRLMKAGAIFAEDRRDYIGIQWKLDMVSLIEI
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     mRNA            join(<1615. .2124,2196. .>3047)
                     /product="hexokinase-t2"
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                     /codon_start=1
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                     /protein_id="AAG22944.1"
                     /db_xref="GI:10765242"
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                     APGEYRNCNKVLSELGILGCQEPDKEALRYICEAVSSRSAKLCACGLVTIINKMNINE
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                     SKL"
ORIGIN

  Query Match             80.0%;  Score 16.8;  DB 3;  Length 3047;
  Best Local Similarity   90.0%;  Pred. No. 3.1e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 CGTCGAACGTTCGAGATGAT 21
              |||||||||  |||  ||||||
Db        156 CGTCGAACGATCGTGATGAT 137


RESULT 14
AF257639/c
LOCUS       AF257639               3047 bp    DNA     linear   INV 09-OCT-2000
DEFINITION  Drosophila simulans strain CT96_5s hexokinase-t1 and hexokinase-t2
            genes, complete cds.
ACCESSION   AF257639
VERSION     AF257639.1  GI:10765246
KEYWORDS    .
SOURCE      Drosophila simulans
  ORGANISM  Drosophila simulans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 3047)
  AUTHORS   Duvernell,D.D. and Eanes,W.F.
  TITLE     Contrasting molecular population genetics of four hexokinases in
            Drosophila melanogaster and Drosophila simulans
  JOURNAL   Genetics (2000) In press
REFERENCE   2  (bases 1 to 3047)
  AUTHORS   Duvernell,D.D. and Eanes,W.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-APR-2000) Ecology and Evolution, State University of
            New York, Stony Brook, NY 11794, USA
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FEATURES             Location/Qualifiers
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                     IMGSIANSCYVERVERCETYEGDEFRRLMIINSDWAHFGDTGQLDFIRNEFDRLLDTD
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                     VSDPPGVYTKAQEVMDKFRIRHCKERDLAALKYICDTVTNRAAMLVASGVSCLIDRMR
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                     SKL"
ORIGIN

  Query Match             80.0%;  Score 16.8;  DB 3;  Length 3047;
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  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 CGTCGAACGTTCGAGATGAT 21
              ||||||||| ||| ||||||
Db        156 CGTCGAACGATCGTGATGAT 137


RESULT 15
AF257640/c
LOCUS       AF257640               3047 bp    DNA     linear   INV 09-OCT-2000
DEFINITION  Drosophila simulans strain CT96_6s hexokinase-t1 and hexokinase-t2
            genes, complete cds.
ACCESSION   AF257640
VERSION     AF257640.1  GI:10765249
KEYWORDS    .
SOURCE      Drosophila simulans
  ORGANISM  Drosophila simulans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 3047)
  AUTHORS   Duvernell,D.D. and Eanes,W.F.
  TITLE     Contrasting molecular population genetics of four hexokinases in
            Drosophila melanogaster and Drosophila simulans
  JOURNAL   Genetics (2000) In press
REFERENCE   2  (bases 1 to 3047)
  AUTHORS   Duvernell,D.D. and Eanes,W.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-APR-2000) Ecology and Evolution, State University of
            New York, Stony Brook, NY 11794, USA
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /strain="CT96_6s"
                     /db_xref="taxon:7240"
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     CDS             1. .1398
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                     SINPGTRIYEKFSGALCMGELVRIIVLRLMKAGAIFAEDRRDYIGIQWKLDMVSLIEI
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                     /product="hexokinase-t2"
     CDS             join(1615. .2124,2196. .3047)
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                     SKL"
ORIGIN

  Query Match             80.0%;  Score 16.8;  DB 3;  Length 3047;
  Best Local Similarity   90.0%;  Pred. No. 3.1e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 CGTCGAACGTTCGAGATGAT 21
              ||||||||| ||| ||||||
Db        156 CGTCGAACGATCGTGATGAT 137


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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY_NUC
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Searched: 4390206 seqs, 2959870667 residues

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Post-processing: Minimum Match 0%
Maximum Match 100%
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12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	21	100.0	21	6	ABQ75182	Abq75182 ISS immun
2	21	100.0	21	12	ADK67599	Adk67599 Immunosti
3	21	100.0	21	13	ADQ16896	Adq16896 Immunomod
4	21	100.0	21	13	ADQ16939	Adq16939 Immunomod
c 5	21	100.0	21	13	ADQ16892	Adq16892 Immunomod
6	21	100.0	21	13	ADQ16924	Adq16924 Immunomod
7	21	100.0	21	13	ADQ16748	Adq16748 Immunomod
8	21	100.0	21	13	ADQ16895	Adq16895 Immunomod
c 9	21	100.0	21	13	ADQ16898	Adq16898 Immunomod
10	21	100.0	21	13	ADQ16901	Adq16901 Immunomod
c 11	21	100.0	21	13	ADQ16922	Adq16922 Immunomod
12	21	100.0	21	13	ADQ16938	Adq16938 Immunomod
13	21	100.0	21	13	ADQ16940	Adq16940 Immunomod
14	21	100.0	21	13	ADQ16894	Adq16894 Immunomod
15	21	100.0	21	13	ADQ16941	Adq16941 Immunomod
16	21	100.0	21	13	ADQ16897	Adq16897 Immunomod
17	21	100.0	21	13	ADQ16893	Adq16893 Immunomod
c 18	20	95.2	21	13	ADQ16750	Adq16750 Immunomod
19	19	90.5	19	6	ABQ75170	Abq75170 ISS immun
20	19	90.5	19	9	ADB88838	Adb88838 Chimeric
21	19	90.5	19	10	ACC49937	Acc49937 Human imm
22	19	90.5	19	12	ADQ95304	Adq95304 Branched
23	19	90.5	19	12	ADQ95303	Adq95303 Branched
24	19	90.5	19	12	ADQ95299	Adq95299 Branched
25	19	90.5	19	13	ADQ16876	Adq16876 Immunomod
26	19	90.5	19	13	ADQ16744	Adq16744 Immunomod
27	19	90.5	22	6	ABQ75181	Abq75181 ISS immun
28	19	90.5	22	9	ADB88849	Adb88849 Chimeric
29	19	90.5	22	12	ADQ95310	Adq95310 Branched
30	19	90.5	22	13	ADQ16745	Adq16745 Immunomod
31	18	85.7	18	13	ADQ16820	Adq16820 Immunomod
32	18	85.7	19	6	ABQ75175	Abq75175 ISS immun
33	18	85.7	19	9	ADB88843	Adb88843 Chimeric
34	18	85.7	19	13	ADQ16743	Adq16743 Immunomod
35	18	85.7	21	13	ADQ16827	Adq16827 Immunomod
36	17.8	84.8	21	13	ADQ16765	Adq16765 Immunomod
37	17.8	84.8	21	13	ADQ16766	Adq16766 Immunomod
38	17.8	84.8	21	13	ADQ16790	Adq16790 Immunomod
39	17.8	84.8	21	13	ADQ16772	Adq16772 Immunomod
40	17.8	84.8	21	13	ADQ16769	Adq16769 Immunomod
41	17.8	84.8	21	13	ADQ16768	Adq16768 Immunomod
42	17.4	82.9	19	6	ABQ75221	Abq75221 ISS immun
43	17.4	82.9	19	6	ABQ75222	Abq75222 ISS immun
44	17.4	82.9	19	9	ADB88891	Adb88891 Chimeric
45	17.4	82.9	19	9	ADB88892	Adb88892 Chimeric

ALIGNMENTS

RESULT 1
ABQ75182
ID ABQ75182 standard; DNA; 21 BP.
XX
AC ABQ75182;
XX
DT 05-NOV-2002 (first entry)
XX
DE ISS immunomodulatory oligonucleotide SEQ ID NO:132.
XX
KW Immunostimulatory sequence; ISS: immunomodulatory; immune response;
KW allergy; asthma; infectious disease; interferon-gamma; IFN-gamma;
KW idiopathic pulmonary fibrosis; viral infection; mycobacterial disease;
KW malaria; leishmaniasis; toxoplasmosis; schistosomiasis; clonorchiasis;
KW immunoglobulin E; IgE-related disorder; antiallergic; antiasthmatic;
KW virucide; antibacterial; protozoacide; ss.
XX
OS Synthetic.
XX
PN WO200252002-A2.
XX
PD 04-JUL-2002.
XX
PF 27-DEC-2001; 2001WO-US050821.
XX
PR 27-DEC-2000; 2000US-0258675P.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Fearon KL, Dina D;
XX
DR WPI; 2002-657426/70.
XX
PT Immunomodulatory polynucleotide for modulating an immune response in a
PT subject suffering from disorders associated with Th2-type immune
PT response, e.g. allergy, or infectious disease, comprises an
PT immunostimulatory sequence.
XX
PS Claim 4; Page 21; 95pp; English.
XX
CC The present invention describes an immunomodulatory polynucleotide (I)
CC comprising an immunostimulatory sequence (ISS). Also described: (1) an
CC immunomodulatory composition comprising (I); (2) an immunomodulatory

CC polynucleotide/microcarrier (IMP/MC) complex, comprising (I) linked to a
CC biodegradable MC, where the MC is less than 10 micrometre in size; and
CC (3) a kit comprising (I). (I) has antiallergic, antiasthmatic, virucide,
CC antibacterial and protozoacide activities, and can be used as a modulator
CC of immune response. (I) is useful for modulating an immune response in an
CC individual suffering from disorders associated with a Th2-type immune
CC response, especially an allergy or asthma, or an infectious disease. (I)
CC is also useful for increasing interferon-gamma (IFN-gamma) in an
CC individual having idiopathic pulmonary fibrosis, or IFN-alpha in an
CC individual having a viral infection. (I) is further useful for
CC ameliorating a symptom of an infectious disease caused by a cellular
CC pathogen such as mycobacterial disease, malaria, leishmaniasis,
CC toxoplasmosis, schistosomiasis and clonorchiasis in an individual, or a
CC symptom of an immunoglobulin E (IgE)-related disorder, preferably an
CC allergy-related disorder, in particular asthma in an individual. The
CC present sequence represents an immunomodulatory oligonucleotide from the
CC present invention
XX
SQ Sequence 21 BP; 5 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGAACGTTCGAGATGAT 21
||||||||||||||||||||
Db 1 TCGTCGAACGTTCGAGATGAT 21

RESULT 2
ADK67599
ID ADK67599 standard; DNA; 21 BP.
XX
AC ADK67599;
XX
DT 06-MAY-2004 (first entry)
XX
DE Immunostimulant oligonucleotide, for immunomodulatory composition.
XX
KW Immunomodulator; immunostimulant; vaccine; ss.
XX
OS Synthetic.
XX
PN WO2004014322-A2.
XX
PD 19-FEB-2004.
XX
PF 12-AUG-2003; 2003WO-US025415.
XX
PR 12-AUG-2002; 2002US-0402968P.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Van Nest G, Tuck S;
XX
DR WPI; 2004-238627/22.
XX
PT Immunomodulatory composition useful for modulating immune responses in
PT individuals, comprises immunomodulatory particles or a particulate
PT composition made by mixing cationic condensing agent and an
PT immunomodulatory compound.
XX
PS Example 6; SEQ ID NO 39; 90pp; English.
XX
CC The present sequence is that of an immunomodulatory compound (IMC) that
CC was used in an example from the invention. Novel immunomodulatory
CC compositions of the invention comprise a cationic condensing agent, an
CC IMC comprising the nucleotide sequence 5'-CG-3', and a stabilising agent.
CC The compositions form particles which have increased immunomodulatory
CC activity as compared to IMCs not formulated in the compositions of the
CC invention. The immunomodulatory compositions can be used for
CC immunomodulation of an individual, e.g. when the individual suffers from
CC a disorder associated with a Th2-type immune response (e.g. allergies or
CC allergy-induced asthma), is receiving vaccines such as therapeutic
CC vaccines (e.g. vaccines comprising an allergy epitope, a mycobacterial
CC epitope or a tumour associated epitope) or prophylactic vaccines, suffers
CC from cancer, suffers from an infectious disease or is at risk of exposure
CC to an infectious agent. In an example from the invention, the present IMC
CC was used to examine the effects of polymyxin particulate formulations on
CC immunostimulant activity in human peripheral blood mononuclear cells, and
CC enhancement of interferon-alpha production from plasmacytoind dendritic
CC cells by IMC particulate formulations.
XX
SQ Sequence 21 BP; 5 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 12; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGAACGTTCGAGATGAT 21
||||||||||||||||||||
Db 1 TCGTCGAACGTTCGAGATGAT 21

RESULT 3
ADQ16896
ID ADQ16896 standard; DNA; 21 BP.
XX
AC ADQ16896;
XX
DT 07-OCT-2004 (first entry)
XX
DE Immunomodulatory polynucleotide, SEQ ID No 190.
XX
KW Immunomodulatory polynucleotide; IMP; palindromic sequence; dinucleotide;
KW trinucleotide; antimicrobial; antiallergic; antiasthmatic;
KW dermatological; antiinflammatory; ophthalmological; immunosuppressive;
KW antibacterial; vasotropic; antiparasitic; virucide; hepatotropic;
KW anti-HIV; cytostatic; antiulcer; nephrotropic; IgE-related disorder;
KW T helper; (TH)2-type immune response; vaccine; prophylactic; immune;
KW interferon-gamma; interferon-alpha; type I interferon; IFN-alpha;
KW IFN-omega; IFN-gamma; plasmacytoid dendritic cell; ss.
XX
OS Unidentified.
XX
PN WO2004058179-A2.
XX
PD 15-JUL-2004.
XX
PF 18-DEC-2003; 2003WO-US041001.
XX
PR 23-DEC-2002; 2002US-0436122P.
PR 13-FEB-2003; 2003US-0447885P.
PR 01-MAY-2003; 2003US-0467546P.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES.
XX
PI Dina D, Fearon KL, Marshall J;
XX
DR WPI; 2004-525782/50.
XX
PT Immunomodulatory polynucleotide useful for the treatment of e.g. atopic
PT dermatitis comprises palindromic sequence comprising at least eight bases
PT in length, which contains at least two dinucleotides and at least one
PT trinucleotide.
XX
PS Example 1; SEQ ID NO 190; 119pp; English.
XX
CC The invention relates to a novel immunomodulatory polynucleotide (IMP)
CC comprising a palindromic sequence. The palindromic sequence comprises at
CC least 8 bases in length, which contains at least two dinucleotides (CG),
CC and at least one trinucleotide (TCG)y at or near the 5' end of the
CC polynucleotide. The CG dinucleotides are separated by 0 - 5 bases. The 5'
CC T of the (TCG)y is positioned 0 - 3 bases from the 5' end of the
CC polynucleotide. The (TCG)y is separated from the 5' end of the
CC palindromic sequence by 0 - 2 bases. The palindromic sequence includes

CC all or part of the (TCG)y sequence, where y= 1 or 2. The immunomodulatory
CC polynucleotides have the following activities: antimicrobial,
CC antiallergic, antiasthmatic, dermatological, antiinflammatory,
CC ophthalmological, immunosuppressive, antibacterial, vasotropic,
CC antiparasitic, virucide, hepatotropic, anti-HIV, cytostatic, antiulcer,
CC and nephrotropic. The immunomodulatory polynucleotides can be used for
CC ameliorating a symptom of an infectious disease and IgE-related disorder.
CC The IMP's may also be used for the treatment of a disorder associated
CC with a T helper (TH)2-type immune response (e.g. allergies, allergy-
CC induced asthma or atopic dermatitis), individuals receiving vaccines such
CC as therapeutic vaccines (e.g. vaccines comprising an allergy epitope, a
CC mycobacterial epitope or a tumour associated epitope) or prophylactic
CC vaccines. The IMP's can also be used for the treatment of e.g. food
CC allergies, rhinitis, atopic dermatitis, conjunctivitis, urticaria, shock,
CC Hymenoptera sting allergies and drug allergies and parasitic infections;
CC viral disease e.g. Hepatitis B, Hepatitis C, influenza, Acquired
CC immunodeficiency syndrome (AIDS) and Herpes zoster; and cancer;
CC inflammatory disorder e.g. ulcerative colitis; fibrotic disorder e.g.
CC idiopathic pulmonary fibrosis, scleroderma, cutaneous radiation-induced
CC fibrosis, hepatic fibrosis including schistosomiasis-induced hepatic
CC fibrosis, renal fibrosis. The IMP's may also be used to create a
CC prophylactic vaccine to increase resistance to infection by bacterial or
CC viral pathogens. The immunomodulatory polynucleotide modulates an immune
CC response; or increases interferon-gamma; or interferon-alpha; effectively
CC stimulates cytokines including type I interferons e.g. IFN-alpha and IFN-
CC omega and IFN-gamma, production from human cells; effectively stimulates
CC B cells to proliferate; and activates plasmacytoid dendritic cells to
CC undergo maturation which can result in retardation of plasmacytoid
CC dendritic cell apoptosis in culture. This polynucleotide sequence
CC represents an immunomodulatory polynucleotide of the invention.
XX
SQ Sequence 21 BP; 5 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 13; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGAACGTTCGAGATGAT 21
||||||||||||||||||||
Db 1 TCGTCGAACGTTCGAGATGAT 21

RESULT 4
ADQ16939
ID ADQ16939 standard; DNA; 21 BP.
XX
AC ADQ16939;
XX
DT 07-OCT-2004 (first entry)
XX
DE Immunomodulatory polynucleotide, SEQ ID No 184.
XX
KW Immunomodulatory polynucleotide; IMP; palindromic sequence; dinucleotide;
KW trinucleotide; antimicrobial; antiallergic; antiasthmatic;
KW dermatological; antiinflammatory; ophthalmological; immunosuppressive;
KW antibacterial; vasotropic; antiparasitic; virucide; hepatotropic;
KW anti-HIV; cytostatic; antiulcer; nephrotropic; IgE-related disorder;
KW T helper; (TH)2-type immune response; vaccine; prophylactic; immune;
KW interferon-gamma; interferon-alpha; type I interferon; IFN-alpha;
KW IFN-omega; IFN-gamma; plasmacytoid dendritic cell; ds.
XX
OS Unidentified.
XX
PN WO2004058179-A2.
XX
PD 15-JUL-2004.
XX
PF 18-DEC-2003; 2003WO-US041001.
XX
PR 23-DEC-2002; 2002US-0436122P.
PR 13-FEB-2003; 2003US-0447885P.
PR 01-MAY-2003; 2003US-0467546P.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES.
XX
PI Dina D, Fearon KL, Marshall J;
XX
DR WPI; 2004-525782/50.
XX
PT Immunomodulatory polynucleotide useful for the treatment of e.g. atopic
PT dermatitis comprises palindromic sequence comprising at least eight bases
PT in length, which contains at least two dinucleotides and at least one
PT trinucleotide.
XX
PS Disclosure; SEQ ID NO 184; 119pp; English.
XX
CC The invention relates to a novel immunomodulatory polynucleotide (IMP)
CC comprising a palindromic sequence. The palindromic sequence comprises at
CC least 8 bases in length, which contains at least two dinucleotides (CG),
CC and at least one trinucleotide (TCG)y at or near the 5' end of the
CC polynucleotide. The CG dinucleotides are separated by 0 - 5 bases. The 5'
CC T of the (TCG)y is positioned 0 - 3 bases from the 5' end of the
CC polynucleotide. The (TCG)y is separated from the 5' end of the
CC palindromic sequence by 0 - 2 bases. The palindromic sequence includes
CC all or part of the (TCG)y sequence, where y= 1 or 2. The immunomodulatory
CC polynucleotides have the following activities: antimicrobial,
CC antiallergic, antiasthmatic, dermatological, antiinflammatory,
CC ophthalmological, immunosuppressive, antibacterial, vasotropic,
CC antiparasitic, virucide, hepatotropic, anti-HIV, cytostatic, antiulcer,
CC and nephrotropic. The immunomodulatory polynucleotides can be used for
CC ameliorating a symptom of an infectious disease and IgE-related disorder.
CC The IMP's may also be used for the treatment of a disorder associated
CC with a T helper (TH)2-type immune response (e.g. allergies, allergy-
CC induced asthma or atopic dermatitis), individuals receiving vaccines such
CC as therapeutic vaccines (e.g. vaccines comprising an allergy epitope, a
CC mycobacterial epitope or a tumour associated epitope) or prophylactic
CC vaccines. The IMP's can also be used for the treatment of e.g. food
CC allergies, rhinitis, atopic dermatitis, conjunctivitis, urticaria, shock,
CC Hymenoptera sting allergies and drug allergies and parasitic infections;
CC viral disease e.g. Hepatitis B, Hepatitis C, influenza, Acquired
CC immunodeficiency syndrome (AIDS) and Herpes zoster; and cancer;
CC inflammatory disorder e.g. ulcerative colitis; fibrotic disorder e.g.
CC idiopathic pulmonary fibrosis, scleroderma, cutaneous radiation-induced
CC fibrosis, hepatic fibrosis including schistosomiasis-induced hepatic
CC fibrosis, renal fibrosis. The IMP's may also be used to create a
CC prophylactic vaccine to increase resistance to infection by bacterial or
CC viral pathogens. The immunomodulatory polynucleotide modulates an immune
CC response; or increases interferon-gamma; or interferon-alpha; effectively
CC stimulates cytokines including type I interferons e.g. IFN-alpha and IFN-
CC omega and IFN-gamma, production from human cells; effectively stimulates
CC B cells to proliferate; and activates plasmacytoid dendritic cells to
CC undergo maturation which can result in retardation of plasmacytoid
CC dendritic cell apoptosis in culture. This polynucleotide sequence
CC represents an immunomodulatory polynucleotide of the invention.
XX
SQ Sequence 21 BP; 5 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 13; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGAACGTTCGAGATGAT 21
||||||||||||||||||||
Db 1 TCGTCGAACGTTCGAGATGAT 21

RESULT 5
ADQ16892/c
ID ADQ16892 standard; DNA; 21 BP.
XX
AC ADQ16892;
XX
DT 07-OCT-2004 (first entry)
XX
DE Immunomodulatory polynucleotide, SEQ ID No 182.
XX

KW Immunomodulatory polynucleotide; IMP; palindromic sequence; dinucleotide;
KW trinucleotide; antimicrobial; antiallergic; antiasthmatic;
KW dermatological; antiinflammatory; ophthalmological; immunosuppressive;
KW antibacterial; vasotropic; antiparasitic; virucide; hepatotropic;
KW anti-HIV; cytostatic; antiulcer; nephrotropic; IgE-related disorder;
KW T helper; (TH)2-type immune response; vaccine; prophylactic; immune;
KW interferon-gamma; interferon-alpha; type I interferon; IFN-alpha;
KW IFN-omega; IFN-gamma; plasmacytoid dendritic cell; ss.
XX
OS Unidentified.
XX
PN WO2004058179-A2.
XX
PD 15-JUL-2004.
XX
PF 18-DEC-2003; 2003WO-US041001.
XX
PR 23-DEC-2002; 2002US-0436122P.
PR 13-FEB-2003; 2003US-0447885P.
PR 01-MAY-2003; 2003US-0467546P.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES.
XX
PI Dina D, Fearon KL, Marshall J;
XX
DR WPI; 2004-525782/50.
XX
PT Immunomodulatory polynucleotide useful for the treatment of e.g. atopic
PT dermatitis comprises palindromic sequence comprising at least eight bases
PT in length, which contains at least two dinucleotides and at least one
PT trinucleotide.
XX
PS Example 1; SEQ ID NO 182; 119pp; English.
XX
CC The invention relates to a novel immunomodulatory polynucleotide (IMP)
CC comprising a palindromic sequence. The palindromic sequence comprises at
CC least 8 bases in length, which contains at least two dinucleotides (CG),
CC and at least one trinucleotide (TCG)y at or near the 5' end of the
CC polynucleotide. The CG dinucleotides are separated by 0 - 5 bases. The 5'
CC T of the (TCG)y is positioned 0 - 3 bases from the 5' end of the
CC polynucleotide. The (TCG)y is separated from the 5' end of the
CC palindromic sequence by 0 - 2 bases. The palindromic sequence includes
CC all or part of the (TCG)y sequence, where y= 1 or 2. The immunomodulatory
CC polynucleotides have the following activities: antimicrobial,
CC antiallergic, antiasthmatic, dermatological, antiinflammatory,
CC ophthalmological, immunosuppressive, antibacterial, vasotropic,
CC antiparasitic, virucide, hepatotropic, anti-HIV, cytostatic, antiulcer,
CC and nephrotropic. The immunomodulatory polynucleotides can be used for
CC ameliorating a symptom of an infectious disease and IgE-related disorder.
CC The IMP's may also be used for the treatment of a disorder associated
CC with a T helper (TH)2-type immune response (e.g. allergies, allergy-
CC induced asthma or atopic dermatitis), individuals receiving vaccines such
CC as therapeutic vaccines (e.g. vaccines comprising an allergy epitope, a
CC mycobacterial epitope or a tumour associated epitope) or prophylactic
CC vaccines. The IMP's can also be used for the treatment of e.g. food
CC allergies, rhinitis, atopic dermatitis, conjunctivitis, urticaria, shock,
CC Hymenoptera sting allergies and drug allergies and parasitic infections;
CC viral disease e.g. Hepatitis B, Hepatitis C, influenza, Acquired
CC immunodeficiency syndrome (AIDS) and Herpes zoster; and cancer;
CC inflammatory disorder e.g. ulcerative colitis; fibrotic disorder e.g.
CC idiopathic pulmonary fibrosis, scleroderma, cutaneous radiation-induced
CC fibrosis, hepatic fibrosis including schistosomiasis-induced hepatic
CC fibrosis, renal fibrosis. The IMP's may also be used to create a
CC prophylactic vaccine to increase resistance to infection by bacterial or
CC viral pathogens. The immunomodulatory polynucleotide modulates an immune
CC response; or increases interferon-gamma; or interferon-alpha; effectively
CC stimulates cytokines including type I interferons e.g. IFN-alpha and IFN-
CC omega and IFN-gamma, production from human cells; effectively stimulates
CC B cells to proliferate; and activates plasmacytoid dendritic cells to
CC undergo maturation which can result in retardation of plasmacytoid
CC dendritic cell apoptosis in culture. This polynucleotide sequence
CC represents an immunomodulatory polynucleotide of the invention.
XX

SQ Sequence 21 BP; 6 A; 6 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 13; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGAACGTTCGAGATGAT 21
||||||||||||||||||||
Db 21 TCGTCGAACGTTCGAGATGAT 1

RESULT 6
ADQ16924
ID ADQ16924 standard; DNA; 21 BP.
XX
AC ADQ16924;
XX
DT 07-OCT-2004 (first entry)
XX
DE Immunomodulatory polynucleotide, SEQ ID No 218.
XX
KW Immunomodulatory polynucleotide; IMP; palindromic sequence; dinucleotide;
KW trinucleotide; antimicrobial; antiallergic; antiasthmatic;
KW dermatological; antiinflammatory; ophthalmological; immunosuppressive;
KW antibacterial; vasotropic; antiparasitic; virucide; hepatotropic;
KW anti-HIV; cytostatic; antiulcer; nephrotropic; IgE-related disorder;
KW T helper; (TH)2-type immune response; vaccine; prophylactic; immune;
KW interferon-gamma; interferon-alpha; type I interferon; IFN-alpha;
KW IFN-omega; IFN-gamma; plasmacytoid dendritic cell; ss.
XX
OS Unidentified.
XX
PN WO2004058179-A2.
XX
PD 15-JUL-2004.
XX
PF 18-DEC-2003; 2003WO-US041001.
XX
PR 23-DEC-2002; 2002US-0436122P.
PR 13-FEB-2003; 2003US-0447885P.
PR 01-MAY-2003; 2003US-0467546P.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES.
XX
PI Dina D, Fearon KL, Marshall J;
XX
DR WPI; 2004-525782/50.
XX
PT Immunomodulatory polynucleotide useful for the treatment of e.g. atopic
PT dermatitis comprises palindromic sequence comprising at least eight bases
PT in length, which contains at least two dinucleotides and at least one
PT trinucleotide.
XX
PS Disclosure; SEQ ID NO 218; 119pp; English.
XX
CC The invention relates to a novel immunomodulatory polynucleotide (IMP)
CC comprising a palindromic sequence. The palindromic sequence comprises at
CC least 8 bases in length, which contains at least two dinucleotides (CG),
CC and at least one trinucleotide (TCG)y at or near the 5' end of the
CC polynucleotide. The CG dinucleotides are separated by 0 - 5 bases. The 5'
CC T of the (TCG)y is positioned 0 - 3 bases from the 5' end of the
CC polynucleotide. The (TCG)y is separated from the 5' end of the
CC palindromic sequence by 0 - 2 bases. The palindromic sequence includes
CC all or part of the (TCG)y sequence, where y= 1 or 2. The immunomodulatory
CC polynucleotides have the following activities: antimicrobial,
CC antiallergic, antiasthmatic, dermatological, antiinflammatory,
CC ophthalmological, immunosuppressive, antibacterial, vasotropic,
CC antiparasitic, virucide, hepatotropic, anti-HIV, cytostatic, antiulcer,
CC and nephrotropic. The immunomodulatory polynucleotides can be used for
CC ameliorating a symptom of an infectious disease and IgE-related disorder.
CC The IMP's may also be used for the treatment of a disorder associated
CC with a T helper (TH)2-type immune response (e.g. allergies, allergy-
CC induced asthma or atopic dermatitis), individuals receiving vaccines such

CC as therapeutic vaccines (e.g. vaccines comprising an allergy epitope, a
CC mycobacterial epitope or a tumour associated epitope) or prophylactic
CC vaccines. The IMP's can also be used for the treatment of e.g. food
CC allergies, rhinitis, atopic dermatitis, conjunctivitis, urticaria, shock,
CC Hymenoptera sting allergies and drug allergies and parasitic infections;
CC viral disease e.g. Hepatitis B, Hepatitis C, influenza, Acquired
CC immunodeficiency syndrome (AIDS) and Herpes zoster; and cancer;
CC inflammatory disorder e.g. ulcerative colitis; fibrotic disorder e.g.
CC idiopathic pulmonary fibrosis, scleroderma, cutaneous radiation-induced
CC fibrosis, hepatic fibrosis including schistosomiasis-induced hepatic
CC fibrosis, renal fibrosis. The IMP's may also be used to create a
CC prophylactic vaccine to increase resistance to infection by bacterial or
CC viral pathogens. The immunomodulatory polynucleotide modulates an immune
CC response; or increases interferon-gamma; or interferon-alpha; effectively
CC stimulates cytokines including type I interferons e.g. IFN-alpha and IFN-
CC omega and IFN-gamma, production from human cells; effectively stimulates
CC B cells to proliferate; and activates plasmacytoid dendritic cells to
CC undergo maturation which can result in retardation of plasmacytoid
CC dendritic cell apoptosis in culture. This polynucleotide sequence
CC represents an immunomodulatory polynucleotide of the invention.
XX
SQ Sequence 21 BP; 5 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 13; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGAACGTTCGAGATGAT 21
||||||||||||||||||||
Db 1 TCGTCGAACGTTCGAGATGAT 21

RESULT 7
ADQ16748
ID ADQ16748 standard; DNA; 21 BP.
XX
AC ADQ16748;
XX
DT 07-OCT-2004 (first entry)
XX
DE Immunomodulatory polynucleotide, SEQ ID No 27.
XX
KW Immunomodulatory polynucleotide; IMP; palindromic sequence; dinucleotide;
KW trinucleotide; antimicrobial; antiallergic; antiasthmatic;
KW dermatological; antiinflammatory; ophthalmological; immunosuppressive;
KW antibacterial; vasotropic; antiparasitic; virucide; hepatotropic;
KW anti-HIV; cytostatic; antiulcer; nephrotropic; IgE-related disorder;
KW T helper; (TH)2-type immune response; vaccine; prophylactic; immune;
KW interferon-gamma; interferon-alpha; type I interferon; IFN-alpha;
KW IFN-omega; IFN-gamma; plasmacytoid dendritic cell; ss.
XX
OS Unidentified.
XX
PN WO2004058179-A2.
XX
PD 15-JUL-2004.
XX
PF 18-DEC-2003; 2003WO-US041001.
XX
PR 23-DEC-2002; 2002US-0436122P.
PR 13-FEB-2003; 2003US-0447885P.
PR 01-MAY-2003; 2003US-0467546P.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES.
XX
PI Dina D, Pearon KL, Marshall J;
XX
DR WPI; 2004-525782/50.
XX
PT Immunomodulatory polynucleotide useful for the treatment of e.g. atopic
PT dermatitis comprises palindromic sequence comprising at least eight bases
PT in length, which contains at least two dinucleotides and at least one
PT trinucleotide.
XX
PS Claim 9; SEQ ID NO 27; 119pp; English.
XX
CC The invention relates to a novel immunomodulatory polynucleotide (IMP)
CC comprising a palindromic sequence. The palindromic sequence comprises at
CC least 8 bases in length, which contains at least two dinucleotides (CG),
CC and at least one trinucleotide (TCG)y at or near the 5' end of the
CC polynucleotide. The CG dinucleotides are separated by 0 - 5 bases. The 5'
CC T of the (TCG)y is positioned 0 - 3 bases from the 5' end of the
CC polynucleotide. The (TCG)y is separated from the 5' end of the
CC palindromic sequence by 0 - 2 bases. The palindromic sequence includes
CC all or part of the (TCG)y sequence, where y= 1 or 2. The immunomodulatory
CC polynucleotides have the following activities: antimicrobial,
CC antiallergic, antiasthmatic, dermatological, antiinflammatory,
CC ophthalmological, immunosuppressive, antibacterial, vasotropic,
CC antiparasitic, virucide, hepatotropic, anti-HIV, cytostatic, antiulcer,
CC and nephrotropic. The immunomodulatory polynucleotides can be used for
CC ameliorating a symptom of an infectious disease and IgE-related disorder.
CC The IMP's may also be used for the treatment of a disorder associated
CC with a T helper (TH)2-type immune response (e.g. allergies, allergy-
CC induced asthma or atopic dermatitis), individuals receiving vaccines such
CC as therapeutic vaccines (e.g. vaccines comprising an allergy epitope, a
CC mycobacterial epitope or a tumour associated epitope) or prophylactic
CC vaccines. The IMP's can also be used for the treatment of e.g. food
CC allergies, rhinitis, atopic dermatitis, conjunctivitis, urticaria, shock,
CC Hymenoptera sting allergies and drug allergies and parasitic infections;
CC viral disease e.g. Hepatitis B, Hepatitis C, influenza, Acquired
CC immunodeficiency syndrome (AIDS) and Herpes zoster; and cancer;
CC inflammatory disorder e.g. ulcerative colitis; fibrotic disorder e.g.
CC idiopathic pulmonary fibrosis, scleroderma, cutaneous radiation-induced
CC fibrosis, hepatic fibrosis including schistosomiasis-induced hepatic
CC fibrosis, renal fibrosis. The IMP's may also be used to create a
CC prophylactic vaccine to increase resistance to infection by bacterial or
CC viral pathogens. The immunomodulatory polynucleotide modulates an immune
CC response; or increases interferon-gamma; or interferon-alpha; effectively
CC stimulates cytokines including type I interferons e.g. IFN-alpha and IFN-
CC omega and IFN-gamma, production from human cells; effectively stimulates
CC B cells to proliferate; and activates plasmacytoid dendritic cells to
CC undergo maturation which can result in retardation of plasmacytoid
CC dendritic cell apoptosis in culture. This polynucleotide sequence
CC represents an immunomodulatory polynucleotide of the invention.
XX
SQ Sequence 21 BP; 5 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 13; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGAACGTTCGAGATGAT 21
||||||||||||||||||||
Db 1 TCGTCGAACGTTCGAGATGAT 21

RESULT 8
ADQ16895
ID ADQ16895 standard; DNA; 21 BP.
XX
AC ADQ16895;
XX
DT 07-OCT-2004 (first entry)
XX
DE Immunomodulatory polynucleotide, SEQ ID No 189.
XX
KW Immunomodulatory polynucleotide; IMP; palindromic sequence; dinucleotide;
KW trinucleotide; antimicrobial; antiallergic; antiasthmatic;
KW dermatological; antiinflammatory; ophthalmological; immunosuppressive;
KW antibacterial; vasotropic; antiparasitic; virucide; hepatotropic;
KW anti-HIV; cytostatic; antiulcer; nephrotropic; IgE-related disorder;
KW T helper; (TH)2-type immune response; vaccine; prophylactic; immune;
KW interferon-gamma; interferon-alpha; type I interferon; IFN-alpha;
KW IFN-omega; IFN-gamma; plasmacytoid dendritic cell; ss.
XX
OS Unidentified.

```
XX
PN   WO2004058179-A2.
XX
PD   15-JUL-2004.
XX
PF   18-DEC-2003; 2003WO-US041001.
XX
PR   23-DEC-2002; 2002US-0436122P.
PR   13-FEB-2003; 2003US-0447885P.
PR   01-MAY-2003; 2003US-0467546P.
XX
PA   (DYNA-) DYNAVAX TECHNOLOGIES.
XX
PI   Dina D,  Fearon KL,  Marshall J;
XX
DR   WPI; 2004-525782/50.
XX
PT   Immunomodulatory polynucleotide useful for the treatment of e.g. atopic
PT   dermatitis comprises palindromic sequence comprising at least eight bases
PT   in length, which contains at least two dinucleotides and at least one
PT   trinucleotide.
XX
PS   Example 1; SEQ ID NO 189; 119pp; English.
XX
CC   The invention relates to a novel immunomodulatory polynucleotide (IMP)
CC   comprising a palindromic sequence. The palindromic sequence comprises at
CC   least 8 bases in length, which contains at least two dinucleotides (CG),
CC   and at least one trinucleotide (TCG)y at or near the 5' end of the
CC   polynucleotide. The CG dinucleotides are separated by 0 - 5 bases. The 5'
CC   T of the (TCG)y is positioned 0 - 3 bases from the 5' end of the
CC   polynucleotide. The (TCG)y is separated from the 5' end of the
CC   palindromic sequence by 0 - 2 bases. The palindromic sequence includes
CC   all or part of the (TCG)y sequence, where y= 1 or 2. The immunomodulatory
CC   polynucleotides have the following activities: antimicrobial,
CC   antiallergic, antiasthmatic, dermatological, antiinflammatory,
CC   ophthalmological, immunosuppressive, antibacterial, vasotropic,
CC   antiparasitic, virucide, hepatotropic, anti-HIV, cytostatic, antiulcer,
CC   and nephrotropic. The immunomodulatory polynucleotides can be used for
CC   ameliorating a symptom of an infectious disease and IgE-related disorder.
CC   The IMP's may also be used for the treatment of a disorder associated
CC   with a T helper (TH)2-type immune response (e.g. allergies, allergy-
CC   induced asthma or atopic dermatitis), individuals receiving vaccines such
CC   as therapeutic vaccines (e.g. vaccines comprising an allergy epitope, a
CC   mycobacterial epitope or a tumour associated epitope) or prophylactic
CC   vaccines. The IMP's can also be used for the treatment of e.g. food
CC   allergies, rhinitis, atopic dermatitis, conjunctivitis, urticaria, shock,
CC   Hymenoptera sting allergies and drug allergies and parasitic infections;
CC   viral disease e.g. Hepatitis B, Hepatitis C, influenza, Acquired
CC   immunodeficiency syndrome (AIDS) and Herpes zoster; and cancer;
CC   inflammatory disorder e.g. ulcerative colitis; fibrotic disorder e.g.
CC   idiopathic pulmonary fibrosis, scleroderma, cutaneous radiation-induced
CC   fibrosis, hepatic fibrosis including schistosomiasis-induced hepatic
CC   fibrosis, renal fibrosis. The IMP's may also be used to create a
CC   prophylactic vaccine to increase resistance to infection by bacterial or
CC   viral pathogens. The immunomodulatory polynucleotide modulates an immune
CC   response; or increases interferon-gamma; or interferon-alpha; effectively
CC   stimulates cytokines including type I interferons e.g. IFN-alpha and IFN-
CC   omega and IFN-gamma, production from human cells; effectively stimulates
CC   B cells to proliferate; and activates plasmacytoid dendritic cells to
CC   undergo maturation which can result in retardation of plasmacytoid
CC   dendritic cell apoptosis in culture. This polynucleotide sequence
CC   represents an immunomodulatory polynucleotide of the invention.
XX
SQ   Sequence 21 BP; 5 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 21;  DB 13;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 0.37;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATGAT 21
              |||||||||||||||||||||
Db          1 TCGTCGAACGTTCGAGATGAT 21
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RESULT 9
ADQ16898/c
ID   ADQ16898 standard; DNA; 21 BP.
XX
AC   ADQ16898;
XX
DT   07-OCT-2004  (first entry)
XX
DE   Immunomodulatory polynucleotide, SEQ ID No 192.
XX
KW   Immunomodulatory polynucleotide; IMP; palindromic sequence; dinucleotide;
KW   trinucleotide; antimicrobial; antiallergic; antiasthmatic;
KW   dermatological; antiinflammatory; ophthalmological; immunosuppressive;
KW   antibacterial; vasotropic; antiparasitic; virucide; hepatotropic;
KW   anti-HIV; cytostatic; antiulcer; nephrotropic; IgE-related disorder;
KW   T helper; (TH)2-type immune response; vaccine; prophylactic; immune;
KW   interferon-gamma; interferon-alpha; type I interferon; IFN-alpha;
KW   IFN-omega; IFN-gamma; plasmacytoid dendritic cell; ss.
XX
OS   Unidentified.
XX
PN   WO2004058179-A2.
XX
PD   15-JUL-2004.
XX
PF   18-DEC-2003; 2003WO-US041001.
XX
PR   23-DEC-2002; 2002US-0436122P.
PR   13-FEB-2003; 2003US-0447885P.
PR   01-MAY-2003; 2003US-0467546P.
XX
PA   (DYNA-) DYNAVAX TECHNOLOGIES.
XX
PI   Dina D,  Fearon KL,  Marshall J;
XX
DR   WPI; 2004-525782/50.
XX
PT   Immunomodulatory polynucleotide useful for the treatment of e.g. atopic
PT   dermatitis comprises palindromic sequence comprising at least eight bases
PT   in length, which contains at least two dinucleotides and at least one
PT   trinucleotide.
XX
PS   Disclosure; SEQ ID NO 192; 119pp; English.
XX
CC   The invention relates to a novel immunomodulatory polynucleotide (IMP)
CC   comprising a palindromic sequence. The palindromic sequence comprises at
CC   least 8 bases in length, which contains at least two dinucleotides (CG),
CC   and at least one trinucleotide (TCG)y at or near the 5' end of the
CC   polynucleotide. The CG dinucleotides are separated by 0 - 5 bases. The 5'
CC   T of the (TCG)y is positioned 0 - 3 bases from the 5' end of the
CC   polynucleotide. The (TCG)y is separated from the 5' end of the
CC   palindromic sequence by 0 - 2 bases. The palindromic sequence includes
CC   all or part of the (TCG)y sequence, where y= 1 or 2. The immunomodulatory
CC   polynucleotides have the following activities: antimicrobial,
CC   antiallergic, antiasthmatic, dermatological, antiinflammatory,
CC   ophthalmological, immunosuppressive, antibacterial, vasotropic,
CC   antiparasitic, virucide, hepatotropic, anti-HIV, cytostatic, antiulcer,
CC   and nephrotropic. The immunomodulatory polynucleotides can be used for
CC   ameliorating a symptom of an infectious disease and IgE-related disorder.
CC   The IMP's may also be used for the treatment of a disorder associated
CC   with a T helper (TH)2-type immune response (e.g. allergies, allergy-
CC   induced asthma or atopic dermatitis), individuals receiving vaccines such
CC   as therapeutic vaccines (e.g. vaccines comprising an allergy epitope, a
CC   mycobacterial epitope or a tumour associated epitope) or prophylactic
CC   vaccines. The IMP's can also be used for the treatment of e.g. food
CC   allergies, rhinitis, atopic dermatitis, conjunctivitis, urticaria, shock,
CC   Hymenoptera sting allergies and drug allergies and parasitic infections;
CC   viral disease e.g. Hepatitis B, Hepatitis C, influenza, Acquired
CC   immunodeficiency syndrome (AIDS) and Herpes zoster; and cancer;
CC   inflammatory disorder e.g. ulcerative colitis; fibrotic disorder e.g.
CC   idiopathic pulmonary fibrosis, scleroderma, cutaneous radiation-induced
CC   fibrosis, hepatic fibrosis including schistosomiasis-induced hepatic
```

CC fibrosis, renal fibrosis. The IMP's may also be used to create a
CC prophylactic vaccine to increase resistance to infection by bacterial or
CC viral pathogens. The immunomodulatory polynucleotide modulates an immune
CC response; or increases interferon-gamma; or interferon-alpha; effectively
CC stimulates cytokines including type I interferons e.g. IFN-alpha and IFN-
CC omega and IFN-gamma, production from human cells; effectively stimulates
CC B cells to proliferate; and activates plasmacytoid dendritic cells to
CC undergo maturation which can result in retardation of plasmacytoid
CC dendritic cell apoptosis in culture. This polynucleotide sequence
CC represents an immunomodulatory polynucleotide of the invention.
XX
SQ Sequence 21 BP; 6 A; 6 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 13; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGAACGTTCGAGATGAT 21
||||||||||||||||||||
Db 21 TCGTCGAACGTTCGAGATGAT 1

RESULT 10
ADQ16901
ID ADQ16901 standard; DNA; 21 BP.
XX
AC ADQ16901;
XX
DT 07-OCT-2004 (first entry)
XX
DE Immunomodulatory polynucleotide, SEQ ID No 195.
XX
KW Immunomodulatory polynucleotide; IMP; palindromic sequence; dinucleotide;
KW trinucleotide; antimicrobial; antiallergic; antiasthmatic;
KW dermatological; antiinflammatory; ophthalmological; immunosuppressive;
KW antibacterial; vasotropic; antiparasitic; virucide; hepatotropic;
KW anti-HIV; cytostatic; antiulcer; nephrotropic; IgE-related disorder;
KW T helper; (TH)2-type immune response; vaccine; prophylactic; immune;
KW interferon-gamma; interferon-alpha; type I interferon; IFN-alpha;
KW IFN-omega; IFN-gamma; plasmacytoid dendritic cell; ss.
XX
OS Unidentified.
XX
PN WO2004058179-A2.
XX
PD 15-JUL-2004.
XX
PF 18-DEC-2003; 2003WO-US041001.
XX
PR 23-DEC-2002; 2002US-0436122P.
PR 13-FEB-2003; 2003US-0447885P.
PR 01-MAY-2003; 2003US-0467546P.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES.
XX
PI Dina D, Fearon KL, Marshall J;
XX
DR WPI; 2004-525782/50.
XX
PT Immunomodulatory polynucleotide useful for the treatment of e.g. atopic
PT dermatitis comprises palindromic sequence comprising at least eight bases
PT in length, which contains at least two dinucleotides and at least one
PT trinucleotide.
XX
PS Disclosure; SEQ ID NO 195; 119pp; English.
XX
CC The invention relates to a novel immunomodulatory polynucleotide (IMP)
CC comprising a palindromic sequence. The palindromic sequence comprises at
CC least 8 bases in length, which contains at least two dinucleotides (CG),
CC and at least one trinucleotide (TCG)y at or near the 5' end of the
CC polynucleotide. The CG dinucleotides are separated by 0 - 5 bases. The 5'
CC T of the (TCG)y is positioned 0 - 3 bases from the 5' end of the
CC polynucleotide. The (TCG)y is separated from the 5' end of the
CC palindromic sequence by 0 - 2 bases. The palindromic sequence includes
CC all or part of the (TCG)y sequence, where y= 1 or 2. The immunomodulatory
CC polynucleotides have the following activities: antimicrobial,
CC antiallergic, antiasthmatic, dermatological, antiinflammatory,
CC ophthalmological, immunosuppressive, antibacterial, vasotropic,
CC antiparasitic, virucide, hepatotropic, anti-HIV, cytostatic, antiulcer,
CC and nephrotropic. The immunomodulatory polynucleotides can be used for
CC ameliorating a symptom of an infectious disease and IgE-related disorder.
CC The IMP's may also be used for the treatment of a disorder associated
CC with a T helper (TH)2-type immune response (e.g. allergies, allergy-
CC induced asthma or atopic dermatitis), individuals receiving vaccines such
CC as therapeutic vaccines (e.g. vaccines comprising an allergy epitope, a
CC mycobacterial epitope or a tumour associated epitope) or prophylactic
CC vaccines. The IMP's can also be used for the treatment of e.g. food
CC allergies, rhinitis, atopic dermatitis, conjunctivitis, urticaria, shock,
CC Hymenoptera sting allergies and drug allergies and parasitic infections;
CC viral disease e.g. Hepatitis B, Hepatitis C, influenza, Acquired
CC immunodeficiency syndrome (AIDS) and Herpes zoster; and cancer;
CC inflammatory disorder e.g. ulcerative colitis; fibrotic disorder e.g.
CC idiopathic pulmonary fibrosis, scleroderma, cutaneous radiation-induced
CC fibrosis, hepatic fibrosis including schistosomiasis-induced hepatic
CC fibrosis, renal fibrosis. The IMP's may also be used to create a
CC prophylactic vaccine to increase resistance to infection by bacterial or
CC viral pathogens. The immunomodulatory polynucleotide modulates an immune
CC response; or increases interferon-gamma; or interferon-alpha; effectively
CC stimulates cytokines including type I interferons e.g. IFN-alpha and IFN-
CC omega and IFN-gamma, production from human cells; effectively stimulates
CC B cells to proliferate; and activates plasmacytoid dendritic cells to
CC undergo maturation which can result in retardation of plasmacytoid
CC dendritic cell apoptosis in culture. This polynucleotide sequence
CC represents an immunomodulatory polynucleotide of the invention.
XX
SQ Sequence 21 BP; 5 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 13; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGAACGTTCGAGATGAT 21
||||||||||||||||||||
Db 1 TCGTCGAACGTTCGAGATGAT 21

RESULT 11
ADQ16922/c
ID ADQ16922 standard; DNA; 21 BP.
XX
AC ADQ16922;
XX
DT 07-OCT-2004 (first entry)
XX
DE Immunomodulatory polynucleotide, SEQ ID No 216.
XX
KW Immunomodulatory polynucleotide; IMP; palindromic sequence; dinucleotide;
KW trinucleotide; antimicrobial; antiallergic; antiasthmatic;
KW dermatological; antiinflammatory; ophthalmological; immunosuppressive;
KW antibacterial; vasotropic; antiparasitic; virucide; hepatotropic;
KW anti-HIV; cytostatic; antiulcer; nephrotropic; IgE-related disorder;
KW T helper; (TH)2-type immune response; vaccine; prophylactic; immune;
KW interferon-gamma; interferon-alpha; type I interferon; IFN-alpha;
KW IFN-omega; IFN-gamma; plasmacytoid dendritic cell; ss.
XX
OS Unidentified.
XX
PN WO2004058179-A2.
XX
PD 15-JUL-2004.
XX
PF 18-DEC-2003; 2003WO-US041001.
XX
PR 23-DEC-2002; 2002US-0436122P.
PR 13-FEB-2003; 2003US-0447885P.
PR 01-MAY-2003; 2003US-0467546P.

XX
PA (DYNA-) DYNAVAX TECHNOLOGIES.
XX
PI Dina D, Fearon KL, Marshall J;
XX
DR WPI; 2004-525782/50.
XX
PT Immunomodulatory polynucleotide useful for the treatment of e.g. atopic
PT dermatitis comprises palindromic sequence comprising at least eight bases
PT in length, which contains at least two dinucleotides and at least one
PT trinucleotide.
XX
PS Disclosure; SEQ ID NO 216; 119pp; English.
XX
CC The invention relates to a novel immunomodulatory polynucleotide (IMP)
CC comprising a palindromic sequence. The palindromic sequence comprises at
CC least 8 bases in length, which contains at least two dinucleotides (CG),
CC and at least one trinucleotide (TCG)y at or near the 5' end of the
CC polynucleotide. The CG dinucleotides are separated by 0 - 5 bases. The 5'
CC T of the (TCG)y is positioned 0 - 3 bases from the 5' end of the
CC polynucleotide. The (TCG)y is separated from the 5' end of the
CC palindromic sequence by 0 - 2 bases. The palindromic sequence includes
CC all or part of the (TCG)y sequence, where y= 1 or 2. The immunomodulatory
CC polynucleotides have the following activities: antimicrobial,
CC antiallergic, antiasthmatic, dermatological, antiinflammatory,
CC ophthalmological, immunosuppressive, antibacterial, vasotropic,
CC antiparasitic, virucide, hepatotropic, anti-HIV, cytostatic, antiulcer,
CC and nephrotropic. The immunomodulatory polynucleotides can be used for
CC ameliorating a symptom of an infectious disease and IgE-related disorder.
CC The IMP's may also be used for the treatment of a disorder associated
CC with a T helper (TH)2-type immune response (e.g. allergies, allergy-
CC induced asthma or atopic dermatitis), individuals receiving vaccines such
CC as therapeutic vaccines (e.g. vaccines comprising an allergy epitope, a
CC mycobacterial epitope or a tumour associated epitope) or prophylactic
CC vaccines. The IMP's can also be used for the treatment of e.g. food
CC allergies, rhinitis, atopic dermatitis, conjunctivitis, urticaria, shock,
CC Hymenoptera sting allergies and drug allergies and parasitic infections;
CC viral disease e.g. Hepatitis B, Hepatitis C, influenza, Acquired
CC immunodeficiency syndrome (AIDS) and Herpes zoster; and cancer;
CC inflammatory disorder e.g. ulcerative colitis; fibrotic disorder e.g.
CC idiopathic pulmonary fibrosis, scleroderma, cutaneous radiation-induced
CC fibrosis, hepatic fibrosis including schistosomiasis-induced hepatic
CC fibrosis, renal fibrosis. The IMP's may also be used to create a
CC prophylactic vaccine to increase resistance to infection by bacterial or
CC viral pathogens. The immunomodulatory polynucleotide modulates an immune
CC response; or increases interferon-gamma; or interferon-alpha; effectively
CC stimulates cytokines including type I interferons e.g. IFN-alpha and IFN-
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CC B cells to proliferate; and activates plasmacytoid dendritic cells to
CC undergo maturation which can result in retardation of plasmacytoid
CC dendritic cell apoptosis in culture. This polynucleotide sequence
CC represents an immunomodulatory polynucleotide of the invention.
XX
SQ Sequence 21 BP; 6 A; 6 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 13; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGAACGTTCGAGATGAT 21
||||||||||||||||||||
Db 21 TCGTCGAACGTTCGAGATGAT 1

RESULT 12
ADQ16938
ID ADQ16938 standard; DNA; 21 BP.
XX
AC ADQ16938;
XX
DT 07-OCT-2004 (first entry)
XX
DE Immunomodulatory polynucleotide, SEQ ID No 183.
XX
KW Immunomodulatory polynucleotide; IMP; palindromic sequence; dinucleotide;
KW trinucleotide; antimicrobial; antiallergic; antiasthmatic;
KW dermatological; antiinflammatory; ophthalmological; immunosuppressive;
KW antibacterial; vasotropic; antiparasitic; virucide; hepatotropic;
KW anti-HIV; cytostatic; antiulcer; nephrotropic; IgE-related disorder;
KW T helper; (TH)2-type immune response; vaccine; prophylactic; immune;
KW interferon-gamma; interferon-alpha; type I interferon; IFN-alpha;
KW IFN-omega; IFN-gamma; plasmacytoid dendritic cell; ds.
XX
OS Unidentified.
XX
PN WO2004058179-A2.
XX
PD 15-JUL-2004.
XX
PF 18-DEC-2003; 2003WO-US041001.
XX
PR 23-DEC-2002; 2002US-0436122P.
PR 13-FEB-2003; 2003US-0447885P.
PR 01-MAY-2003; 2003US-0467546P.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES.
XX
PI Dina D, Fearon KL, Marshall J;
XX
DR WPI; 2004-525782/50.
XX
PT Immunomodulatory polynucleotide useful for the treatment of e.g. atopic
PT dermatitis comprises palindromic sequence comprising at least eight bases
PT in length, which contains at least two dinucleotides and at least one
PT trinucleotide.
XX
PS Disclosure; SEQ ID NO 183; 119pp; English.
XX
CC The invention relates to a novel immunomodulatory polynucleotide (IMP)
CC comprising a palindromic sequence. The palindromic sequence comprises at
CC least 8 bases in length, which contains at least two dinucleotides (CG),
CC and at least one trinucleotide (TCG)y at or near the 5' end of the
CC polynucleotide. The CG dinucleotides are separated by 0 - 5 bases. The 5'
CC T of the (TCG)y is positioned 0 - 3 bases from the 5' end of the
CC polynucleotide. The (TCG)y is separated from the 5' end of the
CC palindromic sequence by 0 - 2 bases. The palindromic sequence includes
CC all or part of the (TCG)y sequence, where y= 1 or 2. The immunomodulatory
CC polynucleotides have the following activities: antimicrobial,
CC antiallergic, antiasthmatic, dermatological, antiinflammatory,
CC ophthalmological, immunosuppressive, antibacterial, vasotropic,
CC antiparasitic, virucide, hepatotropic, anti-HIV, cytostatic, antiulcer,
CC and nephrotropic. The immunomodulatory polynucleotides can be used for
CC ameliorating a symptom of an infectious disease and IgE-related disorder.
CC The IMP's may also be used for the treatment of a disorder associated
CC with a T helper (TH)2-type immune response (e.g. allergies, allergy-
CC induced asthma or atopic dermatitis), individuals receiving vaccines such
CC as therapeutic vaccines (e.g. vaccines comprising an allergy epitope, a
CC mycobacterial epitope or a tumour associated epitope) or prophylactic
CC vaccines. The IMP's can also be used for the treatment of e.g. food
CC allergies, rhinitis, atopic dermatitis, conjunctivitis, urticaria, shock,
CC Hymenoptera sting allergies and drug allergies and parasitic infections;
CC viral disease e.g. Hepatitis B, Hepatitis C, influenza, Acquired
CC immunodeficiency syndrome (AIDS) and Herpes zoster; and cancer;
CC inflammatory disorder e.g. ulcerative colitis; fibrotic disorder e.g.
CC idiopathic pulmonary fibrosis, scleroderma, cutaneous radiation-induced
CC fibrosis, hepatic fibrosis including schistosomiasis-induced hepatic
CC fibrosis, renal fibrosis. The IMP's may also be used to create a
CC prophylactic vaccine to increase resistance to infection by bacterial or
CC viral pathogens. The immunomodulatory polynucleotide modulates an immune
CC response; or increases interferon-gamma; or interferon-alpha; effectively
CC stimulates cytokines including type I interferons e.g. IFN-alpha and IFN-
CC omega and IFN-gamma, production from human cells; effectively stimulates
CC B cells to proliferate; and activates plasmacytoid dendritic cells to
CC undergo maturation which can result in retardation of plasmacytoid
CC dendritic cell apoptosis in culture. This polynucleotide sequence
CC represents an immunomodulatory polynucleotide of the invention.

XX
SQ Sequence 21 BP; 5 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 13; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGAACGTTCGAGATGAT 21
||||||||||||||||||||
Db 1 TCGTCGAACGTTCGAGATGAT 21

RESULT 13
ADQ16940
ID ADQ16940 standard; DNA; 21 BP.
XX
AC ADQ16940;
XX
DT 07-OCT-2004 (first entry)
XX
DE Immunomodulatory polynucleotide, SEQ ID No 185.
XX
KW Immunomodulatory polynucleotide; IMP; palindromic sequence; dinucleotide;
KW trinucleotide; antimicrobial; antiallergic; antiasthmatic;
KW dermatological; antiinflammatory; ophthalmological; immunosuppressive;
KW antibacterial; vasotropic; antiparasitic; virucide; hepatotropic;
KW anti-HIV; cytostatic; antiulcer; nephrotropic; IgE-related disorder;
KW T helper; (TH)2-type immune response; vaccine; prophylactic; immune;
KW interferon-gamma; interferon-alpha; type I interferon; IFN-alpha;
KW IFN-omega; IFN-gamma; plasmacytoid dendritic cell; ds.
XX
OS Unidentified.
XX
PN WO2004058179-A2.
XX
PD 15-JUL-2004.
XX
PF 18-DEC-2003; 2003WO-US041001.
XX
PR 23-DEC-2002; 2002US-0436122P.
PR 13-FEB-2003; 2003US-0447885P.
PR 01-MAY-2003; 2003US-0467546P.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES.
XX
PI Dina D, Fearon KL, Marshall J;
XX
DR WPI; 2004-525782/50.
XX
PT Immunomodulatory polynucleotide useful for the treatment of e.g. atopic
PT dermatitis comprises palindromic sequence comprising at least eight bases
PT in length, which contains at least two dinucleotides and at least one
PT trinucleotide.
XX
PS Disclosure; SEQ ID NO 185; 119pp; English.
XX
CC The invention relates to a novel immunomodulatory polynucleotide (IMP)
CC comprising a palindromic sequence. The palindromic sequence comprises at
CC least 8 bases in length, which contains at least two dinucleotides (CG),
CC and at least one trinucleotide (TCG)y at or near the 5' end of the
CC polynucleotide. The CG dinucleotides are separated by 0 - 5 bases. The 5'
CC T of the (TCG)y is positioned 0 - 3 bases from the 5' end of the
CC polynucleotide. The (TCG)y is separated from the 5' end of the
CC palindromic sequence by 0 - 2 bases. The palindromic sequence includes
CC all or part of the (TCG)y sequence, where y= 1 or 2. The immunomodulatory
CC polynucleotides have the following activities: antimicrobial,
CC antiallergic, antiasthmatic, dermatological, antiinflammatory,
CC ophthalmological, immunosuppressive, antibacterial, vasotropic,
CC antiparasitic, virucide, hepatotropic, anti-HIV, cytostatic, antiulcer,
CC and nephrotropic. The immunomodulatory polynucleotides can be used for
CC ameliorating a symptom of an infectious disease and IgE-related disorder.
CC The IMP's may also be used for the treatment of a disorder associated
CC with a T helper (TH)2-type immune response (e.g. allergies, allergy-
CC induced asthma or atopic dermatitis), individuals receiving vaccines such
CC as therapeutic vaccines (e.g. vaccines comprising an allergy epitope, a
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CC vaccines. The IMP's can also be used for the treatment of e.g. food
CC allergies, rhinitis, atopic dermatitis, conjunctivitis, urticaria, shock,
CC Hymenoptera sting allergies and drug allergies and parasitic infections;
CC viral disease e.g. Hepatitis B, Hepatitis C, influenza, Acquired
CC immunodeficiency syndrome (AIDS) and Herpes zoster; and cancer;
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CC B cells to proliferate; and activates plasmacytoid dendritic cells to
CC undergo maturation which can result in retardation of plasmacytoid
CC dendritic cell apoptosis in culture. This polynucleotide sequence
CC represents an immunomodulatory polynucleotide of the invention.
XX
SQ Sequence 21 BP; 5 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 13; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGAACGTTCGAGATGAT 21
||||||||||||||||||||
Db 1 TCGTCGAACGTTCGAGATGAT 21

RESULT 14
ADQ16894
ID ADQ16894 standard; DNA; 21 BP.
XX
AC ADQ16894;
XX
DT 07-OCT-2004 (first entry)
XX
DE Immunomodulatory polynucleotide, SEQ ID No 188.
XX
KW Immunomodulatory polynucleotide; IMP; palindromic sequence; dinucleotide;
KW trinucleotide; antimicrobial; antiallergic; antiasthmatic;
KW dermatological; antiinflammatory; ophthalmological; immunosuppressive;
KW antibacterial; vasotropic; antiparasitic; virucide; hepatotropic;
KW anti-HIV; cytostatic; antiulcer; nephrotropic; IgE-related disorder;
KW T helper; (TH)2-type immune response; vaccine; prophylactic; immune;
KW interferon-gamma; interferon-alpha; type I interferon; IFN-alpha;
KW IFN-omega; IFN-gamma; plasmacytoid dendritic cell; ss.
XX
OS Unidentified.
XX
PN WO2004058179-A2.
XX
PD 15-JUL-2004.
XX
PF 18-DEC-2003; 2003WO-US041001.
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PR 23-DEC-2002; 2002US-0436122P.
PR 13-FEB-2003; 2003US-0447885P.
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XX
PA (DYNA-) DYNAVAX TECHNOLOGIES.
XX
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CC viral disease e.g. Hepatitis B, Hepatitis C, influenza, Acquired
CC immunodeficiency syndrome (AIDS) and Herpes zoster; and cancer;
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CC response; or increases interferon-gamma; or interferon-alpha; effectively
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Query Match 100.0%; Score 21; DB 13; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGAACGTTCGAGATGAT 21
||||||||||||||||||||
Db 1 TCGTCGAACGTTCGAGATGAT 21

RESULT 15
ADQ16941
ID ADQ16941 standard; DNA; 21 BP.
XX
AC ADQ16941;
XX
DT 07-OCT-2004 (first entry)
XX
DE Immunomodulatory polynucleotide, SEQ ID No 186.
XX
KW Immunomodulatory polynucleotide; IMP; palindromic sequence; dinucleotide;
KW trinucleotide; antimicrobial; antiallergic; antiasthmatic;
KW dermatological; antiinflammatory; ophthalmological; immunosuppressive;
KW antibacterial; vasotropic; antiparasitic; virucide; hepatotropic;
KW anti-HIV; cytostatic; antiulcer; nephrotropic; IgE-related disorder;
KW T helper; (TH)2-type immune response; vaccine; prophylactic; immune;
KW interferon-gamma; interferon-alpha; type I interferon; IFN-alpha;
KW IFN-omega; IFN-gamma; plasmacytoid dendritic cell; ds.
XX
OS Unidentified.
XX
PN WO2004058179-A2.
XX
PD 15-JUL-2004.
XX
PF 18-DEC-2003; 2003WO-US041001.
XX
PR 23-DEC-2002; 2002US-0436122P.
PR 13-FEB-2003; 2003US-0447885P.
PR 01-MAY-2003; 2003US-0467546P.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES.
XX
PI Dina D, Fearon KL, Marshall J;
XX
DR WPI; 2004-525782/50.
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PT in length, which contains at least two dinucleotides and at least one
PT trinucleotide.
XX
PS Disclosure; SEQ ID NO 186; 119pp; English.
XX
CC The invention relates to a novel immunomodulatory polynucleotide (IMP)
CC comprising a palindromic sequence. The palindromic sequence comprises at
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CC polynucleotide. The CG dinucleotides are separated by 0 - 5 bases. The 5'
CC T of the (TCG)y is positioned 0 - 3 bases from the 5' end of the
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CC antiallergic, antiasthmatic, dermatological, antiinflammatory,
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CC as therapeutic vaccines (e.g. vaccines comprising an allergy epitope, a
CC mycobacterial epitope or a tumour associated epitope) or prophylactic
CC vaccines. The IMP's can also be used for the treatment of e.g. food
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CC viral disease e.g. Hepatitis B, Hepatitis C, influenza, Acquired
CC immunodeficiency syndrome (AIDS) and Herpes zoster; and cancer;
CC inflammatory disorder e.g. ulcerative colitis; fibrotic disorder e.g.
CC idiopathic pulmonary fibrosis, scleroderma, cutaneous radiation-induced
CC fibrosis, hepatic fibrosis including schistosomiasis-induced hepatic
CC fibrosis, renal fibrosis. The IMP's may also be used to create a
CC prophylactic vaccine to increase resistance to infection by bacterial or
CC viral pathogens. The immunomodulatory polynucleotide modulates an immune
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CC B cells to proliferate; and activates plasmacytoid dendritic cells to
CC undergo maturation which can result in retardation of plasmacytoid
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CC represents an immunomodulatory polynucleotide of the invention.
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SQ Sequence 21 BP; 5 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 13; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGAACGTTCGAGATGAT 21
||||||||||||||||||||
Db 1 TCGTCGAACGTTCGAGATGAT 21

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RESULT 16
ADQ16897
ID   ADQ16897 standard; DNA; 21 BP.
XX
AC   ADQ16897;
XX
DT   07-OCT-2004  (first entry)
XX
DE   Immunomodulatory polynucleotide, SEQ ID No 191.
XX
KW   Immunomodulatory polynucleotide; IMP; palindromic sequence; dinucleotide;
KW   trinucleotide; antimicrobial; antiallergic; antiasthmatic;
KW   dermatological; antiinflammatory; ophthalmological; immunosuppressive;
KW   antibacterial; vasotropic; antiparasitic; virucide; hepatotropic;
KW   anti-HIV; cytostatic; antiulcer; nephrotropic; IgE-related disorder;
KW   T helper; (TH)2-type immune response; vaccine; prophylactic; immune;
KW   interferon-gamma; interferon-alpha; type I interferon; IFN-alpha;
KW   IFN-omega; IFN-gamma; plasmacytoid dendritic cell; ss.
XX
OS   Unidentified.
XX
PN   WO2004058179-A2.
XX
PD   15-JUL-2004.
XX
PF   18-DEC-2003; 2003WO-US041001.
XX
PR   23-DEC-2002; 2002US-0436122P.
PR   13-FEB-2003; 2003US-0447885P.
PR   01-MAY-2003; 2003US-0467546P.
XX
PA   (DYNA-) DYNAVAX TECHNOLOGIES.
XX
PI   Dina D,  Fearon KL,  Marshall J;
XX
DR   WPI; 2004-525782/50.
XX
PT   Immunomodulatory polynucleotide useful for the treatment of e.g. atopic
PT   dermatitis comprises palindromic sequence comprising at least eight bases
PT   in length, which contains at least two dinucleotides and at least one
PT   trinucleotide.
XX
PS   Disclosure; SEQ ID NO 191; 119pp; English.
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CC   and at least one trinucleotide (TCG)y at or near the 5' end of the
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CC   T of the (TCG)y is positioned 0 - 3 bases from the 5' end of the
CC   polynucleotide. The (TCG)y is separated from the 5' end of the
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CC   all or part of the (TCG)y sequence, where y= 1 or 2. The immunomodulatory
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CC   ameliorating a symptom of an infectious disease and IgE-related disorder.
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CC   dendritic cell apoptosis in culture. This polynucleotide sequence
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SQ   Sequence 21 BP; 5 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 21;  DB 13;  Length 21;
  Best Local Similarity  100.0%;  Pred. No. 0.37;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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              |||||||||||||||||||||
Db          1 TCGTCGAACGTTCGAGATGAT 21


RESULT 17
ADQ16893
ID   ADQ16893 standard; DNA; 21 BP.
XX
AC   ADQ16893;
XX
DT   07-OCT-2004  (first entry)
XX
DE   Immunomodulatory polynucleotide, SEQ ID No 187.
XX
KW   Immunomodulatory polynucleotide; IMP; palindromic sequence; dinucleotide;
KW   trinucleotide; antimicrobial; antiallergic; antiasthmatic;
KW   dermatological; antiinflammatory; ophthalmological; immunosuppressive;
KW   antibacterial; vasotropic; antiparasitic; virucide; hepatotropic;
KW   anti-HIV; cytostatic; antiulcer; nephrotropic; IgE-related disorder;
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KW   IFN-omega; IFN-gamma; plasmacytoid dendritic cell; ss.
XX
OS   Unidentified.
XX
PN   WO2004058179-A2.
XX
PD   15-JUL-2004.
XX
PF   18-DEC-2003; 2003WO-US041001.
XX
PR   23-DEC-2002; 2002US-0436122P.
PR   13-FEB-2003; 2003US-0447885P.
PR   01-MAY-2003; 2003US-0467546P.
XX
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XX
PI   Dina D,  Fearon KL,  Marshall J;
XX
DR   WPI; 2004-525782/50.
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Qy 1 TCGTCGAACGTTCGAGATGAT 21
||||||||||||||||||||
Db 1 TCGTCGAACGTTCGAGATGAT 21

Search completed: March 30, 2005, 14:03:31
Job time : 427 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 30, 2005, 10:06:13 ; Search time 75 Seconds
(without alignments)
458.157 Million cell updates/sec

Title: US-10-033-243-132
Perfect score: 21
Sequence: 1 tcgtcgaacgttcgagatgat 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	16.4	78.1	23	4	US-09-296-477-4	Sequence 4, Appli
c	2	16.2	77.1	3135	4	US-09-107-532A-1575	Sequence 1575, Ap
	3	15.4	73.3	816	3	US-08-776-251-10	Sequence 10, Appl
c	4	15.4	73.3	816	3	US-08-776-251-10	Sequence 10, Appl
c	5	15.4	73.3	1900	4	US-09-555-000-1	Sequence 1, Appli
	6	15.4	73.3	100990	4	US-09-409-800B-2	Sequence 2, Appli
	7	15.2	72.4	342	4	US-09-134-000C-2551	Sequence 2551, Ap
c	8	15.2	72.4	1938	4	US-09-710-279-2983	Sequence 2983, Ap
c	9	15.2	72.4	3097	4	US-09-710-279-3781	Sequence 3781, Ap
	10	15.2	72.4	3188	4	US-09-710-279-3837	Sequence 3837, Ap
	11	15.2	72.4	3594	4	US-09-710-279-3803	Sequence 3803, Ap
c	12	15.2	72.4	3641	4	US-09-710-279-3851	Sequence 3851, Ap
c	13	15.2	72.4	3707	4	US-09-949-016-3912	Sequence 3912, Ap
c	14	15.2	72.4	4506	4	US-09-710-279-2849	Sequence 2849, Ap
c	15	15.2	72.4	4590	3	US-09-134-001C-1108	Sequence 1108, Ap
	16	15	71.4	22	4	US-09-235-742-19	Sequence 19, Appl
	17	15	71.4	22	4	US-09-347-343-32	Sequence 32, Appl
	18	15	71.4	22	4	US-09-820-484-1	Sequence 1, Appli
	19	15	71.4	22	4	US-09-820-484-3	Sequence 3, Appli
	20	15	71.4	22	4	US-09-774-403A-1	Sequence 1, Appli
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	24	15	71.4	22	4	US-09-308-036A-1	Sequence 1, Appli
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	26	15	71.4	22	4	US-09-565-906-2	Sequence 2, Appli
	27	14.8	70.5	813	4	US-09-107-532A-1566	Sequence 1566, Ap
	28	14.8	70.5	1069	4	US-09-374-174B-1	Sequence 1, Appli
	29	14.8	70.5	1497	4	US-09-252-991A-2256	Sequence 2256, Ap
c	30	14.8	70.5	1950	4	US-09-252-991A-2425	Sequence 2425, Ap
	31	14.8	70.5	2799	1	US-08-446-794A-5	Sequence 5, Appli
	32	14.8	70.5	2799	1	US-08-750-007-4	Sequence 4, Appli
	33	14.6	69.5	424	4	US-09-621-976-12664	Sequence 12664, A
	34	14.6	69.5	3468	3	US-09-221-017B-893	Sequence 893, App
	35	14.6	69.5	144362	4	US-09-949-016-16066	Sequence 16066, A
	36	14.4	68.6	77	1	US-08-399-412A-58	Sequence 58, Appl
c	37	14.4	68.6	209	4	US-09-270-767-9743	Sequence 9743, Ap
c	38	14.4	68.6	209	4	US-09-270-767-25025	Sequence 25025, A
	39	14.4	68.6	601	4	US-09-949-016-142803	Sequence 142803,
	40	14.4	68.6	1737	4	US-09-470-667-3	Sequence 3, Appli
	41	14.4	68.6	1740	4	US-09-470-667-1	Sequence 1, Appli
	42	14.4	68.6	1740	4	US-09-470-667-4	Sequence 4, Appli
	43	14.4	68.6	80411	4	US-09-949-016-15777	Sequence 15777, A
	44	14.2	67.6	77	1	US-08-447-169A-36	Sequence 36, Appl
	45	14.2	67.6	77	2	US-08-233-012C-36	Sequence 36, Appl

ALIGNMENTS

RESULT 1
US-09-296-477-4/c
; Sequence 4, Application US/09296477A
; Patent No. 6589940
; GENERAL INFORMATION:
; APPLICANT: RAZ, E.
; APPLICANT: SCHWARTZ, D.
; APPLICANT: ROMAN, M.
; APPLICANT: DINA, D.
; TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGONUCLEOTIDES,
; TITLE OF INVENTION: COMPOSITIONS THEREOF AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 377882000420
; CURRENT APPLICATION NUMBER: US/09/296,477A
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: 09/092,329
; EARLIER FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: 60/048,793
; EARLIER FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-09-296-477-4

Query Match 78.1%; Score 16.4; DB 4; Length 23;
Best Local Similarity 94.4%; Pred. No. 17;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          3 GTCGAACGTTCGAGATGA 20
              || ||||||||||||||||
Db         18 GTGGAACGTTCGAGATGA 1
```

RESULT 2
US-09-107-532A-1575/c
; Sequence 1575, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street

```
;              CITY: Waltham
;              STATE: Massachusetts
;              COUNTRY: USA
;              ZIP: 02354
;         COMPUTER READABLE FORM:
;              MEDIUM TYPE: CD/ROM ISO9660
;              COMPUTER: PC
;              OPERATING SYSTEM: <Unknown>
;              SOFTWARE: ASCII
;         CURRENT APPLICATION DATA:
;              APPLICATION NUMBER: US/09/107,532A
;              FILING DATE: 30-Jun-1998
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: 60/085,598
;              FILING DATE: 14 May 1998
;              APPLICATION NUMBER: 60/051571
;              FILING DATE: July 2, 1997
;         ATTORNEY/AGENT INFORMATION:
;              NAME: Ariniello, Pamela Deneke
;              REGISTRATION NUMBER: 40,489
;              REFERENCE/DOCKET NUMBER: GTC-012
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: (781)893-5007
;              TELEFAX: (781)893-8277
;    INFORMATION FOR SEQ ID NO: 1575:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 3135 base pairs
;              TYPE: nucleic acid
;              STRANDEDNESS: double
;              TOPOLOGY: circular
;         MOLECULE TYPE: DNA (genomic)
;         HYPOTHETICAL: NO
;         ANTI-SENSE: NO
;         ORIGINAL SOURCE:
;              ORGANISM: Enterococcus faecium
;         FEATURE:
;              NAME/KEY:  misc_feature
;              LOCATION: (B) LOCATION 1...3135
;         SEQUENCE DESCRIPTION: SEQ ID NO: 1575:
US-09-107-532A-1575

  Query Match             77.1%;  Score 16.2;  DB 4;  Length 3135;
  Best Local Similarity   85.7%;  Pred. No. 42;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATGAT 21
              ||||  ||||||  ||||||||
Db       2725 TCGTTAAACGTTGGAGATGAT 2705


RESULT 3
US-08-776-251-10
; Sequence 10, Application US/08776251
; Patent No. 6025340
;  GENERAL INFORMATION:
;    APPLICANT:  Springer, Caroline J
;    APPLICANT:  Marais, Richard
;    TITLE OF INVENTION:  Surface expression of enzyme in gene directed prodrug therapy
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Nixon & Vanderhye
;      STREET:  1100 No. 6025340th Glebe Road, 8th Floor
;      CITY:  Arlington
;      STATE:  Virginia
;      COUNTRY:  USA
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/776,251
;      FILING DATE:  31-JAN-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB95/01782
;      FILING DATE:  27-JUL-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9415167.7
;      FILING DATE:  27-JUL-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Arthur R. Crawford
;      REGISTRATION NUMBER:  25,327
;      REFERENCE/DOCKET NUMBER:  620-20
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  816 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-776-251-10

  Query Match             73.3%;  Score 15.4;  DB 3;  Length 816;
  Best Local Similarity   94.1%;  Pred. No. 95;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 TCGAACGTTCGAGATGA 20
              |||||||||||||| ||
Db        619 TCGAACGTTCGAGACGA 635


RESULT 4
US-08-776-251-10/c
; Sequence 10, Application US/08776251
; Patent No. 6025340
;  GENERAL INFORMATION:
;    APPLICANT:  Springer, Caroline J
;    APPLICANT:  Marais, Richard
;    TITLE OF INVENTION:  Surface expression of enzyme in gene directed prodrug therapy
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Nixon & Vanderhye
;      STREET:  1100 No. 6025340th Glebe Road, 8th Floor
;      CITY:  Arlington
;      STATE:  Virginia
;      COUNTRY:  USA
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/776,251
;      FILING DATE:  31-JAN-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB95/01782
;      FILING DATE:  27-JUL-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9415167.7
;      FILING DATE:  27-JUL-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Arthur R. Crawford
;      REGISTRATION NUMBER:  25,327
;      REFERENCE/DOCKET NUMBER:  620-20
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  816 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-776-251-10

  Query Match             73.3%;  Score 15.4;  DB 3;  Length 816;
  Best Local Similarity   94.1%;  Pred. No. 95;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
```

```
Qy          4 TCGAACGTTCGAGATGA 20
              ||||||||||||||| ||
Db        630 TCGAACGTTCGAGACGA 614
```

RESULT 5
US-09-555-000-1/c
; Sequence 1, Application US/09555000
; Patent No. 6489108
; GENERAL INFORMATION:
; APPLICANT: Genencor International, Inc.
; TITLE OF INVENTION: Proteases from Gram Positive Organisms
; FILE REFERENCE: GC390-PCT
; CURRENT APPLICATION NUMBER: US/09/555,000
; CURRENT FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: PCT/US98/26971
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1900
; TYPE: DNA
; ORGANISM: Bacillus subtilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (134)...(1774)
US-09-555-000-1

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  Query Match             73.3%;  Score 15.4;  DB 4;  Length 1900;
  Best Local Similarity   94.1%;  Pred. No. 1.1e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 CGAACGTTCGAGATGAT 21
              |||||||||||| |||||
Db       1119 CGAACGTTCGACATGAT 1103
```

RESULT 6
US-09-409-800B-2
; Sequence 2, Application US/09409800B
; Patent No. 6706522
; GENERAL INFORMATION:
; APPLICANT: Blattner, Frederick R.
; APPLICANT: Burland, Valerie
; APPLICANT: Rose, Debra J.
; APPLICANT: Mayhew, George F.
; APPLICANT: Perna, Nicole
; APPLICANT: Perry, Robert D.
; APPLICANT: Straley, Susan C.
; APPLICANT: Fetherston, Jacqueline D.
; APPLICANT: Lindler, Luther E.
; APPLICANT: Plano, Gregory V.
; TITLE OF INVENTION: Plasmid DNA From Yersinia Pestis
; FILE REFERENCE: 960296.95939
; CURRENT APPLICATION NUMBER: US/09/409,800B
; CURRENT FILING DATE: 1999-09-30
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 100990
; TYPE: DNA
; ORGANISM: Yersinia pestis
US-09-409-800B-2

```
  Query Match             73.3%;  Score 15.4;  DB 4;  Length 100990;
  Best Local Similarity   94.1%;  Pred. No. 1.8e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 TCGAACGTTCGAGATGA 20
              |||| ||||||||||||
Db      91915 TCGACCGTTCGAGATGA 91931
```

RESULT 7
US-09-134-000C-2551
; Sequence 2551, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2551
; LENGTH: 342
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-2551

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  Query Match             72.4%;  Score 15.2;  DB 4;  Length 342;
  Best Local Similarity   85.0%;  Pred. No. 1.1e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATGA 20
              |||||||| ||||  |||||
Db         31 TCGTCGAAGGTTCCTGATGA 50
```

RESULT 8
US-09-710-279-2983/c
; Sequence 2983, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2983
; LENGTH: 1938
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-09-710-279-2983

```
  Query Match             72.4%;  Score 15.2;  DB 4;  Length 1938;
  Best Local Similarity   85.0%;  Pred. No. 1.4e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 CGTCGAACGTTCGAGATGAT 21
              ||||||||||  ||| |||
Db        945 CGTCGAACGTTGAAGAAGAT 926
```

RESULT 9
US-09-710-279-3781/c
; Sequence 3781, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09

```
;  PRIOR APPLICATION NUMBER: 60/164,258
;  PRIOR FILING DATE: 1999-11-09
;  NUMBER OF SEQ ID NOS: 4472
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3781
;   LENGTH: 3097
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: nucleic acid sequence
US-09-710-279-3781

  Query Match             72.4%;  Score 15.2;  DB 4;  Length 3097;
  Best Local Similarity   85.0%;  Pred. No. 1.5e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 CGTCGAACGTTCGAGATGAT 21
              ||||||||||  ||| |||
Db        111 CGTCGAACGTTGAAGAAGAT 92


RESULT 10
US-09-710-279-3837
; Sequence 3837, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
;  APPLICANT: KIMMERLY, WILLIAM JOHN
;  TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
;  FILE REFERENCE: PU3480US
;  CURRENT APPLICATION NUMBER: US/09/710,279
;  CURRENT FILING DATE:  2000-11-09
;  PRIOR APPLICATION NUMBER: 60/164,258
;  PRIOR FILING DATE: 1999-11-09
;  NUMBER OF SEQ ID NOS: 4472
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3837
;   LENGTH: 3188
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: nucleic acid sequence
US-09-710-279-3837

  Query Match             72.4%;  Score 15.2;  DB 4;  Length 3188;
  Best Local Similarity   85.0%;  Pred. No. 1.5e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 CGTCGAACGTTCGAGATGAT 21
              ||||||||||  ||| |||
Db        292 CGTCGAACGTTGAAGAAGAT 311


RESULT 11
US-09-710-279-3803
; Sequence 3803, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
;  APPLICANT: KIMMERLY, WILLIAM JOHN
;  TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
;  FILE REFERENCE: PU3480US
;  CURRENT APPLICATION NUMBER: US/09/710,279
;  CURRENT FILING DATE:  2000-11-09
;  PRIOR APPLICATION NUMBER: 60/164,258
;  PRIOR FILING DATE: 1999-11-09
;  NUMBER OF SEQ ID NOS: 4472
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3803
;   LENGTH: 3594
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: nucleic acid sequence
US-09-710-279-3803

  Query Match             72.4%;  Score 15.2;  DB 4;  Length 3594;
  Best Local Similarity   85.0%;  Pred. No. 1.5e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 CGTCGAACGTTCGAGATGAT 21
              ||||||||||  ||| |||
Db       2100 CGTCGAACGTTGAAGAAGAT 2119


RESULT 12
US-09-710-279-3851/c
; Sequence 3851, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
;  APPLICANT: KIMMERLY, WILLIAM JOHN
;  TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
;  FILE REFERENCE: PU3480US
;  CURRENT APPLICATION NUMBER: US/09/710,279
;  CURRENT FILING DATE:  2000-11-09
;  PRIOR APPLICATION NUMBER: 60/164,258
;  PRIOR FILING DATE: 1999-11-09
;  NUMBER OF SEQ ID NOS: 4472
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3851
;   LENGTH: 3641
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: nucleic acid sequence
US-09-710-279-3851

  Query Match             72.4%;  Score 15.2;  DB 4;  Length 3641;
  Best Local Similarity   85.0%;  Pred. No. 1.5e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 CGTCGAACGTTCGAGATGAT 21
              ||||||||||  ||| |||
Db       1563 CGTCGAACGTTGAAGAAGAT 1544


RESULT 13
US-09-949-016-3912/c
; Sequence 3912, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3912
;   LENGTH: 3707
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-3912

  Query Match             72.4%;  Score 15.2;  DB 4;  Length 3707;
  Best Local Similarity   85.0%;  Pred. No. 1.5e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;
```

```
Qy          2 CGTCGAACGTTCGAGATGAT 21
              | |||||| || ||||||||
Db        450 CCTCGAACCTTGGAGATGAT 431


RESULT 14
US-09-710-279-2849/c
; Sequence 2849, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
;  APPLICANT: KIMMERLY, WILLIAM JOHN
;  TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
;  FILE REFERENCE: PU3480US
;  CURRENT APPLICATION NUMBER: US/09/710,279
;  CURRENT FILING DATE:  2000-11-09
;  PRIOR APPLICATION NUMBER: 60/164,258
;  PRIOR FILING DATE: 1999-11-09
;  NUMBER OF SEQ ID NOS: 4472
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2849
;   LENGTH: 4506
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: nucleic acid sequence
US-09-710-279-2849

  Query Match             72.4%;  Score 15.2;  DB 4;  Length 4506;
  Best Local Similarity   85.0%;  Pred. No. 1.5e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 CGTCGAACGTTCGAGATGAT 21
              |||||||||||  ||| |||
Db       3513 CGTCGAACGTTGAAGAAGAT 3494


RESULT 15
US-09-134-001C-1108/c
; Sequence 1108, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
;  APPLICANT: Lynn Doucette-Stamm et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
;  TITLE OF INVENTION:  EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: GTC-007
;  CURRENT APPLICATION NUMBER: US/09/134,001C
;  CURRENT FILING DATE:  1998-08-13
;  PRIOR APPLICATION NUMBER: US 60/064,964
;  PRIOR FILING DATE: 1997-11-08
;  PRIOR APPLICATION NUMBER: US 60/055,779
;  PRIOR FILING DATE: 1997-08-14
;  NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 1108
;   LENGTH: 4590
;   TYPE: DNA
;   ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1108

  Query Match             72.4%;  Score 15.2;  DB 3;  Length 4590;
  Best Local Similarity   85.0%;  Pred. No. 1.5e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 CGTCGAACGTTCGAGATGAT 21
              |||||||||||  ||| |||
Db       3597 CGTCGAACGTTGAAGAAGAT 3578


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Job time : 76 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 30, 2005, 10:45:07 ; Search time 3117 Seconds
(without alignments)
256.448 Million cell updates/sec

Title: US-10-033-243-132
Perfect score: 21
Sequence: 1 tcgtcgaacgttcgagatgat 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
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Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
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5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	18.4	87.6	802	9	CNS04SNV	AL305428 Tetraodon
	2	17.8	84.8	302	6	CD182992	CD182992 MS1-0037T
c	3	17.8	84.8	441	6	CD156376	CD156376 ML1-0046T
	4	17.8	84.8	586	6	CD124255	CD124255 ME1-0086G
c	5	17.8	84.8	785	7	CF434519	CF434519 EST670864
	6	16.8	80.0	221	6	CD572389	CD572389 PBL_20_H0
c	7	16.8	80.0	382	7	CV043005	dba13c12.
c	8	16.8	80.0	461	6	CA707068	CA707068 wdk2c.pk0
	9	16.8	80.0	587	6	CA827269	CA827269 1114012C1
c	10	16.8	80.0	595	8	BH387860	BH387860 AG-ND-129
	11	16.8	80.0	1410	2	BE052250	BE052250 GA__Ea003
c	12	16.4	78.1	303	2	AW710594	AW710594 e4h01ne.r
	13	16.4	78.1	424	5	BW170465	BW170465
	14	16.4	78.1	439	4	BI515898	BI515898 BB160020B
c	15	16.4	78.1	445	5	BW300285	BW300285 BW300285
c	16	16.4	78.1	457	5	BP018564	BP018564 BP018564
c	17	16.4	78.1	504	8	B29433	B29433 F19L12TFB I
	18	16.4	78.1	511	4	BI514876	BI514876 BB160016B
	19	16.4	78.1	511	4	BI514893	BI514893 BB160016B
	20	16.4	78.1	570	5	BP539000	BP539000 BP539000
	21	16.4	78.1	635	5	BW118728	BW118728 BW118728
	22	16.4	78.1	650	1	AV902415	AV902415 AV902415
	23	16.4	78.1	662	5	BW174317	BW174317 BW174317
	24	16.4	78.1	663	5	BW171245	BW171245 BW171245
	25	16.4	78.1	666	5	BW414321	BW414321 BW414321
c	26	16.4	78.1	707	5	BW297679	BW297679 BW297679
c	27	16.4	78.1	709	5	BW303599	BW303599 BW303599
	28	16.4	78.1	711	5	BW461330	BW461330 BW461330
	29	16.4	78.1	726	5	BW174467	BW174467 BW174467
c	30	16.4	78.1	727	5	BW437262	BW437262 BW437262
	31	16.4	78.1	767	5	BW502366	BW502366 BW502366
	32	16.4	78.1	914	9	CNS04AO0	AL282105 Tetraodon
	33	16.4	78.1	941	7	CO013173	CO013173 EST801508
	34	16.4	78.1	1197	9	AG427158	AG427158 Mus muscu
	35	16.4	78.1	1660	9	AG430921	AG430921 Mus muscu
	36	16.2	77.1	166	6	CA196886	CA196886 SCBFAD109
c	37	16.2	77.1	273	4	BG931701	BG931701 h112-118
c	38	16.2	77.1	314	6	CD190559	CD190559 MS1-0064U
	39	16.2	77.1	315	6	CD183371	CD183371 MS1-0038U
	40	16.2	77.1	328	4	BI075646	BI075646 IP1_23_C0
c	41	16.2	77.1	329	6	CD177754	CD177754 MS1-0011T
c	42	16.2	77.1	342	6	CD092357	CD092357 MC1-0096T
	43	16.2	77.1	352	7	CN141822	CN141822 WOUND1_2_
	44	16.2	77.1	370	9	CL728886	CL728886 OR_BBa006
	45	16.2	77.1	371	7	CN135967	CN135967 OX1_40_B0

ALIGNMENTS

RESULT 1
CNS04SNV
LOCUS CNS04SNV 802 bp DNA linear GSS 01-SEP-2000
DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone 007J10 of library H from Tetraodon nigroviridis, genomic survey sequence.
ACCESSION AL305428
VERSION AL305428.1 GI:8197678
KEYWORDS GSS; genome survey sequence.
SOURCE Tetraodon nigroviridis
ORGANISM Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetradontoidea; Tetraodontidae; Tetraodon.
REFERENCE 1
AUTHORS Roest Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.
TITLE Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence
JOURNAL Nat. Genet. 25 (2), 235-238 (2000)
MEDLINE 20296633
PUBMED 10835645
REFERENCE 2
AUTHORS Roest Crollius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C., Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.
TITLE Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
JOURNAL Genome Res. 10 (7), 939-949 (2000)
MEDLINE 20359837
PUBMED 10899143
REFERENCE 3 (bases 1 to 802)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
FEATURES Location/Qualifiers
source 1. .802
/organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"

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                     /db_xref="taxon:99883"
                     /clone="007J10"
                     /clone_lib="H"
                     /note="Genoscope sequence ID : C0BH007DE05XD1~end : T7"
ORIGIN

  Query Match             87.6%;  Score 18.4;  DB 9;  Length 802;
  Best Local Similarity   95.0%;  Pred. No. 30;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CGTCGAACGTTCGAGATGAT 21
              |||||||||| |||||||||
Db        623 CGTCGAACGTGCGAGATGAT 642


RESULT 2
CD182992
LOCUS       CD182992                302 bp    mRNA    linear   EST 14-SEP-2003
DEFINITION  MS1-0037T-D120-A09-U.G MS1-0037 Schistosoma mansoni cDNA clone
            MS1-0037T-D120-A09.G, mRNA sequence.
ACCESSION   CD182992
VERSION     CD182992.1  GI:34713214
KEYWORDS    EST.
SOURCE      Schistosoma mansoni
  ORGANISM  Schistosoma mansoni
            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
            Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE   1  (bases 1 to 302)
  AUTHORS   Verjovski-Almeida,S., DeMarco,R., Martins,E.A.L., Guimaraes,P.E.M.,
            Ojopi,E.P.B., Paquola,A.C.M., Piazza,J.P., Nishiyama,M.Y. Jr.,
            Kitajima,J.P., Adamson,R.E., Ashton,P.D., Bonaldo,M.F.,
            Coulson,P.S., Dillon,G.P., Farias,L.P., Gregorio,S.P., Ho,P.L.,
            Leite,R.A., Malaquias,L.C.C., Marques,R.C.P., Miyasato,P.A.,
            Nascimento,A.L.T.O., Ohlweiler,F.P., Reis,E.M., Ribeiro,M.A.,
            Sa,R.G., Stukart,G.C., Soares,M.B., Gargioni,C., Kawano,T.,
            Rodrigues,V., Madeira,A.M.B.N., Wilson,R.A., Menck,C.F.M.,
            Setubal,J.C., Leite,L.C.C. and Dias-Neto,E.
  TITLE     Transcriptome analysis of the acoelomate human parasite Schistosoma
            mansoni
  JOURNAL   Nat. Genet. 35 (2), 148-157 (2003)
  MEDLINE   22879926
   PUBMED   12973350
COMMENT     Contact: Dr. Sergio Verjovski-Almeida
            Departamento de Bioquimica
            Instituto de Quimica - Universidade de Sao Paulo
            Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 Sao Paulo - SP,
            Brasil
            Tel: +55-11-3091-2173
            Fax: +55-11-3091-2186
            Email: verjo@iq.usp.br
            This sequence was derived from the FAPESP Schistosoma mansoni EST
            Genome Project. All sequences in the project were assembled and
            annotated. This entry and all the assembled sequences can be seen
            in the following URL http://bioinfo.iq.usp.br/schisto/
            Plate: MS1-0037T-D120  row: 9  column: A.
FEATURES             Location/Qualifiers
     source          1. .302
                     /organism="Schistosoma mansoni"
                     /mol_type="mRNA"
                     /db_xref="taxon:6183"
                     /clone="MS1-0037T-D120-A09.G"
                     /sex="mixed pool"
                     /dev_stage="schistosomulum"
                     /lab_host="in vitro culture"
                     /clone_lib="MS1-0037"
                     /note="Vector: pGEM T-easy"
ORIGIN

  Query Match             84.8%;  Score 17.8;  DB 6;  Length 302;
  Best Local Similarity   90.5%;  Pred. No. 58;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATGAT 21
              |||||||||||| | ||||||
Db         19 TCGTCGAACGTTTGTGATGAT 39


RESULT 3
CD156376/c
LOCUS       CD156376                441 bp    mRNA    linear   EST 14-SEP-2003
DEFINITION  ML1-0046T-M209-C11-U.G ML1-0046 Schistosoma mansoni cDNA clone
            ML1-0046T-M209-C11.G, mRNA sequence.
ACCESSION   CD156376
VERSION     CD156376.1  GI:34693161
KEYWORDS    EST.
SOURCE      Schistosoma mansoni
  ORGANISM  Schistosoma mansoni
            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
            Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE   1  (bases 1 to 441)
  AUTHORS   Verjovski-Almeida,S., DeMarco,R., Martins,E.A.L., Guimaraes,P.E.M.,
            Ojopi,E.P.B., Paquola,A.C.M., Piazza,J.P., Nishiyama,M.Y. Jr.,
            Kitajima,J.P., Adamson,R.E., Ashton,P.D., Bonaldo,M.F.,
            Coulson,P.S., Dillon,G.P., Farias,L.P., Gregorio,S.P., Ho,P.L.,
            Leite,R.A., Malaquias,L.C.C., Marques,R.C.P., Miyasato,P.A.,
            Nascimento,A.L.T.O., Ohlweiler,F.P., Reis,E.M., Ribeiro,M.A.,
            Sa,R.G., Stukart,G.C., Soares,M.B., Gargioni,C., Kawano,T.,
            Rodrigues,V., Madeira,A.M.B.N., Wilson,R.A., Menck,C.F.M.,
            Setubal,J.C., Leite,L.C.C. and Dias-Neto,E.
  TITLE     Transcriptome analysis of the acoelomate human parasite Schistosoma
            mansoni
  JOURNAL   Nat. Genet. 35 (2), 148-157 (2003)
  MEDLINE   22879926
   PUBMED   12973350
COMMENT     Contact: Dr. Sergio Verjovski-Almeida
            Departamento de Bioquimica
            Instituto de Quimica - Universidade de Sao Paulo
            Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 Sao Paulo - SP,
            Brasil
            Tel: +55-11-3091-2173
            Fax: +55-11-3091-2186
            Email: verjo@iq.usp.br
            This sequence was derived from the FAPESP Schistosoma mansoni EST
            Genome Project. All sequences in the project were assembled and
            annotated. This entry and all the assembled sequences can be seen
            in the following URL http://bioinfo.iq.usp.br/schisto/
            Plate: ML1-0046T-M209  row: 11  column: C.
FEATURES             Location/Qualifiers
     source          1. .441
                     /organism="Schistosoma mansoni"
                     /mol_type="mRNA"
                     /db_xref="taxon:6183"
                     /clone="ML1-0046T-M209-C11.G"
                     /sex="mixed pool"
                     /dev_stage="miracidium"
                     /clone_lib="ML1-0046"
                     /note="Vector: pGEM T-easy"
ORIGIN

  Query Match             84.8%;  Score 17.8;  DB 6;  Length 441;
  Best Local Similarity   90.5%;  Pred. No. 61;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATGAT 21
              |||||||||||| | ||||||
Db        376 TCGTCGAACGTTTGTGATGAT 356


RESULT 4
CD124255
LOCUS       CD124255                586 bp    mRNA    linear   EST 14-SEP-2003
DEFINITION  ME1-0086G-A185-H02-U.B ME1-0086 Schistosoma mansoni cDNA clone
            ME1-0086G-A185-H02.B, mRNA sequence.
ACCESSION   CD124255
VERSION     CD124255.1  GI:34662288
KEYWORDS    EST.
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SOURCE      Schistosoma mansoni
  ORGANISM  Schistosoma mansoni
            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
            Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE   1  (bases 1 to 586)
  AUTHORS   Verjovski-Almeida,S., DeMarco,R., Martins,E.A.L., Guimaraes,P.E.M.,
            Ojopi,E.P.B., Paquola,A.C.M., Piazza,J.P., Nishiyama,M.Y. Jr.,
            Kitajima,J.P., Adamson,R.E., Ashton,P.D., Bonaldo,M.F.,
            Coulson,P.S., Dillon,G.P., Farias,L.P., Gregorio,S.P., Ho,P.L.,
            Leite,R.A., Malaquias,L.C.C., Marques,R.C.P., Miyasato,P.A.,
            Nascimento,A.L.T.O., Ohlweiler,F.P., Reis,E.M., Ribeiro,M.A.,
            Sa,R.G., Stukart,G.C., Soares,M.B., Gargioni,C., Kawano,T.,
            Rodrigues,V., Madeira,A.M.B.N., Wilson,R.A., Menck,C.F.M.,
            Setubal,J.C., Leite,L.C.C. and Dias-Neto,E.
  TITLE     Transcriptome analysis of the acoelomate human parasite Schistosoma
            mansoni
  JOURNAL   Nat. Genet. 35 (2), 148-157 (2003)
  MEDLINE   22879926
   PUBMED   12973350
COMMENT     Contact: Dr. Sergio Verjovski-Almeida
            Departamento de Bioquimica
            Instituto de Quimica - Universidade de Sao Paulo
            Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 Sao Paulo - SP,
            Brasil
            Tel: +55-11-3091-2173
            Fax: +55-11-3091-2186
            Email: verjo@iq.usp.br
            This sequence was derived from the FAPESP Schistosoma mansoni EST
            Genome Project. All sequences in the project were assembled and
            annotated. This entry and all the assembled sequences can be seen
            in the following URL http://bioinfo.iq.usp.br/schisto/
            Plate: ME1-0086G-A185  row: 2  column: H.
FEATURES             Location/Qualifiers
     source          1. .586
                     /organism="Schistosoma mansoni"
                     /mol_type="mRNA"
                     /db_xref="taxon:6183"
                     /clone="ME1-0086G-A185-H02.B"
                     /sex="mixed pool"
                     /dev_stage="egg"
                     /lab_host="Mus musculus"
                     /clone_lib="ME1-0086"
                     /note="Vector: pGEM T-easy"
ORIGIN

  Query Match             84.8%;  Score 17.8;  DB 6;  Length 586;
  Best Local Similarity   90.5%;  Pred. No. 63;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATGAT 21
              ||||||||||||  | ||||||
Db        373 TCGTCGAACGTTTGTGATGAT 393


RESULT 5
CF434519/c
LOCUS       CF434519                785 bp    mRNA    linear   EST 04-SEP-2003
DEFINITION  EST670864 normalized cDNA library of onion Allium cepa cDNA clone
            ACAAA82, mRNA sequence.
ACCESSION   CF434519
VERSION     CF434519.1  GI:34457209
KEYWORDS    EST.
SOURCE      Allium cepa (onion)
  ORGANISM  Allium cepa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Alliaceae;
            Allium.
REFERENCE   1  (bases 1 to 785)
  AUTHORS   Havey,M.J., Cheung,F., Van Aken,S., Utterback,T. and Town,C.D.
  TITLE     Expressed Sequence Tags from a normalized library of mixed onion
            tissues (Allium cepa)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Havey MJ
            Department of Horticulture
            USDA-ARS and University of Wisconsin
            1575 Linden Drive, Madison, WI 53706, USA
            Tel: 608-262-1830
            Fax: 608-262-4743
            Email: mjhavey@facstaff.wisc.edu
            TIGR sequence name ACAAA82TR. For more information:
            http://haveylab.hort.wisc.edu
            Seq primer: CAG GAA ACA GCT ATG ACC.
FEATURES             Location/Qualifiers
     source          1. .785
                     /organism="Allium cepa"
                     /mol_type="mRNA"
                     /cultivar="Red Creole(bulbs), unknown(callus), Ebano &
                     Texas Legend(roots)"
                     /db_xref="taxon:4679"
                     /clone="ACAAA82"
                     /tissue_type="Callus, roots, and young bulbs"
                     /clone_lib="normalized cDNA library of onion"
                     /note="Vector: pCMVSport6.1-ccdb (Invitrogen); Site_1:
                     EcoRV (5'); Site_2: NotI (3'); Equal molar amounts of mRNA
                     from callus, roots, and young bulbs were combined to
                     synthesize the library. Normalization to enrich for
                     low-copy transcripts was performed by proprietary
                     techniques of Invitrogen."
ORIGIN

  Query Match             84.8%;  Score 17.8;  DB 7;  Length 785;
  Best Local Similarity   90.5%;  Pred. No. 65;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATGAT 21
              ||||| ||||||||||||||
Db         65 TTGTCGATCGTTCGAGATGAT 45


RESULT 6
CD572389
LOCUS       CD572389                221 bp    mRNA    linear   EST 12-JUN-2003
DEFINITION  PBL_20_H02 Porcine Brain Library Sus scrofa cDNA clone PBL 5', mRNA
            sequence.
ACCESSION   CD572389
VERSION     CD572389.1  GI:31663456
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 221)
  AUTHORS   Nobis,W., Ren,X., Suchyta,S.P., Suchyta,T.R., Zanella,A.J. and
            Coussens,P.M.
  TITLE     Development of a porcine brain cDNA library, EST database and
            microarray resource
  JOURNAL   Physiol. Genomics 16 (1), 153-159 (2003)
COMMENT     Contact: Paul Coussens
            Michigan State University
            1205H Anthony Hall, East Lansing, MI 48824, USA
            Email: coussens@msu.edu
            Seq primer: M13.
FEATURES             Location/Qualifiers
     source          1. .221
                     /organism="Sus scrofa"
                     /mol_type="mRNA"
                     /db_xref="taxon:9823"
                     /clone="PBL"
                     /sex="male and female"
                     /tissue_type="Brain and central nervous system"
                     /dev_stage="fetal, 10-day, 21-day, 5-week, mature boar,
                     post-pubertal gilt, lactating sow"
                     /clone_lib="Porcine Brain Library"
                     /note="Porcine (Pig) brain library includes pre-frontal
                     cortex, frontal  cortex, hippocampus, hypothalamus,
                     parietal cortex, amygdala,  cerebellum, spinal cord, eye,
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                    accumbens, and fetal pig CNS"
ORIGIN

  Query Match             80.0%;  Score 16.8;  DB 6;  Length 221;
  Best Local Similarity   90.0%;  Pred. No. 2e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 CGTCGAACGTTCGAGATGAT 21
              |||||||| || ||||||||
Db         33 CGTCGAACTTTTGAGATGAT 52


RESULT 7
CV043005/c
LOCUS       CV043005                382 bp    mRNA    linear   EST 23-AUG-2004
DEFINITION  dba13c12.y1 Drosophila simulans testis pSport1 library Drosophila
            simulans cDNA 5' similar to TR:Q9VBF1 Q9VBF1 CG5443 PROTEIN. ;,
            mRNA sequence.
ACCESSION   CV043005
VERSION     CV043005.1  GI:51500544
KEYWORDS    EST.
SOURCE      Drosophila simulans
  ORGANISM  Drosophila simulans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 382)
  AUTHORS   Langley,C., Begun,D., Clifton,S., Pape,D., Marra,M., Hillier,L.,
            Martin,J., Wylie,T., Dante,M., Theising,B., Bowers,Y., Gibbons,M.,
            Ronko,I., Tsagareishvili,R., Ritter,E., Kennedy,S., Waterston,R.
            and Wilson,R.
  TITLE     Drosophila simulans genome project
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Charles Langley, David Begun
            Drosophila simulans genome project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Library materials provided by: Rob Kulathinal (Harvard University)
            & Willie Swanson (University of Washington) Library constructed by:
            Willie Swanson, University of Washington Library re-arrayed by: Rob
            Kulathinal, Harvard University DNA sequencing by: Washington
            University Genome Sequencing Center
            Seq primer: -40RP
            High quality sequence stop: 345.
FEATURES             Location/Qualifiers
     source          1. .382
                     /organism="Drosophila simulans"
                     /mol_type="mRNA"
                     /db_xref="taxon:7240"
                     /lab_host="E. coli DH5-alpha"
                     /clone_lib="Drosophila simulans testis pSport1 library"
                     /note="Vector: pSPORT (BRL); Site_1: NotI; Site_2: SalI;
                     1st strand cDNA was primed with a NotI-oligo(dT) primer.
                     SalI adaptors were ligated following 2nd strand synthesis.
                     Library not normalized."
ORIGIN

  Query Match             80.0%;  Score 16.8;  DB 7;  Length 382;
  Best Local Similarity   90.0%;  Pred. No. 2.2e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 CGTCGAACGTTCGAGATGAT 21
              ||||||||| ||| ||||||
Db         25 CGTCGAACGATCGTGATGAT 6


RESULT 8
CA707068/c
LOCUS       CA707068                461 bp    mRNA    linear   EST 26-NOV-2002
DEFINITION  wdk2c.pk0004.g12 wdk2c Triticum aestivum cDNA clone
            wdk2c.pk0004.g12 5' end, mRNA sequence.
ACCESSION   CA707068
VERSION     CA707068.1  GI:25428861
KEYWORDS    EST.
SOURCE      Triticum aestivum (bread wheat)
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 461)
  AUTHORS   Tingey,S.V., Powell,W., Wolters,P., Dolan,M., Hainey,C., Yuan,Z.,
            Miao,G., Caraher,N. and Hanafey,M.K.
  TITLE     DuPont Wheat cDNA Sequence
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Scott V. Tingey
            Crop Genetics
            E. I. DuPont de Nemours and Company
            1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
            Tel: 302-631-2602
            Fax: 302-631-2607
            Email: Scott.V.Tingey@USA.dupont.com
            Seq primer: M13.
FEATURES             Location/Qualifiers
     source          1. .461
                     /organism="Triticum aestivum"
                     /mol_type="mRNA"
                     /db_xref="taxon:4565"
                     /clone="wdk2c.pk0004.g12"
                     /tissue_type="kernel"
                     /clone_lib="wdk2c"
                     /note="Vector: pBluescript SK+; Site_1: EcoRI; Site_2:
                     XhoI; Wheat (Triticum aestivum L.) developing kernel, 7
                     days after anthesis."
ORIGIN

  Query Match             80.0%;  Score 16.8;  DB 6;  Length 461;
  Best Local Similarity   90.0%;  Pred. No. 2.2e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 CGTCGAACGTTCGAGATGAT 21
              || |||||||| ||||||||
Db        293 CGGCGAACGTTGGAGATGAT 274
      :

RESULT 9
CA827269
LOCUS       CA827269                587 bp    mRNA    linear   EST 11-DEC-2002
DEFINITION  1114012C10.y1 1114 - Unigene IV from Maize Genome Project Zea mays
            cDNA, mRNA sequence.
ACCESSION   CA827269
VERSION     CA827269.1  GI:26455686
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 587)
  AUTHORS   Walbot,V.
  TITLE     Maize ESTs from various cDNA libraries sequenced at Stanford
            University
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 1114012  row: C  column: 10.
FEATURES             Location/Qualifiers
     source          1. .587
                     /organism="Zea mays"
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/mol_type="mRNA"
/db_xref="dbEST:3524_1_56_1_G06.y_1"
/db_xref="taxon:4577"
/clone_lib="1114 - Unigene IV from Maize Genome Project"
/note="This library represents the unique genes found in the fourth round of EST sequencing at Stanford University for the maize genome project. Sequences are present from libraries 1091 and 3524. Contigs were assembled using ZmDBAssembler and 2 representatives from each contig were selected for the Unigene set. All singlets were also selected."

ORIGIN

Query Match 80.0%; Score 16.8; DB 6; Length 587;
Best Local Similarity 90.0%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TCGTCGAACGTTCGAGATGA 20
||||| | ||||||||||||
Db 30 TCGTCCAGCGTTCGAGATGA 49

RESULT 10
BH387860/c
LOCUS BH387860 595 bp DNA linear GSS 11-DEC-2001
DEFINITION AG-ND-129F22.TF ND-TAM Anopheles gambiae genomic clone AG-ND-129F22, genomic survey sequence.
ACCESSION BH387860
VERSION BH387860.1 GI:17334001
KEYWORDS GSS.
SOURCE Anopheles gambiae (African malaria mosquito)
ORGANISM Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
REFERENCE 1 (bases 1 to 595)
AUTHORS Hong,Y.S., Hogan,J.R., Wang,X., Sarkar,A., Sim,C., Loftus,B.J., Ren,C., Huff,E.R., Carlile,J.L., Black,K., Zhang,H.-B., Gardner,M.J. and Collins,F.H.
TITLE Construction of a BAC library and generation of BAC end sequence-tagged connectors for genome sequencing of the African malaria mosquito Anopheles gambiae
JOURNAL Mol. Genet. Genomics 268 (6), 720-728 (2003)
MEDLINE 22542063
PUBMED 12655398
COMMENT Other_GSSs: AG-ND-129F22.TR
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjloftus@tigr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by F.H. Collins and sequenced by The Institute for Genomic Research (TIGR). The BAC library was generated from A. gambiae PEST strain DNA. All DNA was extracted from newly hatched first instar larvae to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&M Universty BAC Center University, College Station, Texas 77843-2123, USA using a HindIII partial digest.
Seq primer: M13 For
Class: BAC ends.
FEATURES Location/Qualifiers
source 1. .595
/organism="Anopheles gambiae"
/mol_type="genomic DNA"
/strain="PEST"
/db_xref="taxon:7165"
/clone="AG-ND-129F22"
/clone_lib="ND-TAM"
/note="Vector: pECBAC1; Site_1: HindIII"

ORIGIN

Query Match 80.0%; Score 16.8; DB 8; Length 595;
Best Local Similarity 90.0%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TCGTCGAACGTTCGAGATGA 20
|||| ||||||| |||||||
Db 177 TCGTGGAACGTTGGAGATGA 158

RESULT 11
BE052250
LOCUS BE052250 1410 bp mRNA linear EST 08-MAR-2001
DEFINITION GA__Ea0035L13f Gossypium arboreum 7-10 dpa fiber library Gossypium arboreum cDNA clone GA__Ea0035L13f, mRNA sequence.
ACCESSION BE052250
VERSION BE052250.1 GI:8379306
KEYWORDS EST.
SOURCE Gossypium arboreum
ORGANISM Gossypium arboreum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
REFERENCE 1 (bases 1 to 1410)
AUTHORS Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J., Henry,D., Wood,T.C., Leslie,A. and Wilkins,T.A.
TITLE An integrated analysis of the genetics, development, and evolution of the cotton fiber
JOURNAL Unpublished (2000)
COMMENT Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: TAATACGACTCACTATAGGG
High quality sequence start: 13
High quality sequence stop: 501.
FEATURES Location/Qualifiers
source 1. .1410
/organism="Gossypium arboreum"
/mol_type="mRNA"
/strain="AKA"
/cultivar="8400"
/db_xref="taxon:29729"
/clone="GA__Ea0035L13f"
/tissue_type="Fibers isolated from bolls harvested 7-10 dpa"
/lab_host="E. coli"
/clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"

ORIGIN

Query Match 80.0%; Score 16.8; DB 2; Length 1410;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TCGTCGAACGTTCGAGATGA 20
|||||||||| ||||||||
Db 1356 TCGTCGAACGAGCGAGATGA 1375

RESULT 12
AW710594/c
LOCUS AW710594 303 bp mRNA linear EST 25-APR-2000
DEFINITION e4h01ne.r1 Neurospora crassa evening cDNA library Neurospora crassa cDNA clone e4h01ne 3', mRNA sequence.
ACCESSION AW710594
VERSION AW710594.1 GI:7599686
KEYWORDS EST.
SOURCE Neurospora crassa

```
  ORGANISM  Neurospora crassa
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
REFERENCE   1  (bases 1 to 303)
  AUTHORS   Zhu,H., Lai,H., Kupfer,D., Dunlap,J.C. and Roe,B.A.
  TITLE     Two Neurospora crassa EST Databases
  JOURNAL   Unpublished (1998)
COMMENT     Other_ESTs: e4h01ne.f1
            Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
            Department of Chemistry and Biochemistry
            Advanced Center for Genome Technology, University of Oklahoma
            620 Parrington Oval, Norman, OK 73019, USA
            Tel: 405 325 4912
            Fax: 405 325 7762
            Email: broe@ou.edu
            Seq primer: Universal Reverse Primer
            High quality sequence stop: 255.
FEATURES             Location/Qualifiers
     source          1. .303
                     /organism="Neurospora crassa"
                     /mol_type="mRNA"
                     /strain="Strain 30-7 (bd; A)"
                     /db_xref="taxon:5141"
                     /clone="e4h01ne"
                     /tissue_type="tissue harvested following 22hr growth in
                     dark"
                     /clone_lib="Neurospora crassa evening cDNA library"
                     /note="Vector: pBlueScript SK-; Site_1: XbaI; Site_2:
                     EcoRI; See: Bell-Perdersen,D., et al. PNAS 93:13096,1996.
                     5' end of cDNA cloned into XbaI site of pBluescript; 3'
                     end of cDNA cloned into EcoRI site of pBluescript"
ORIGIN

  Query Match             78.1%;  Score 16.4;  DB 2;  Length 303;
  Best Local Similarity   94.4%;  Pred. No. 3.5e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 GTCGAACGTTCGAGATGA 20
              |||||||||| ||||||
Db        232 GTCGAACGTTCAAGATGA 215


RESULT 13
BW170465
LOCUS       BW170465                424 bp    mRNA    linear   EST 04-NOV-2002
DEFINITION  BW170465 Nori Satoh unpublished cDNA library, neural complex Ciona
            intestinalis cDNA clone rcinc008n07 3', mRNA sequence.
ACCESSION   BW170465
VERSION     BW170465.1  GI:24560352
KEYWORDS    EST.
SOURCE      Ciona intestinalis
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 424)
  AUTHORS   Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
  TITLE     Expressed genes in Ciona intestinalis (2002c)
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .424
                     /organism="Ciona intestinalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:7719"
                     /clone="rcinc008n07"
                     /tissue_type="neural complex"
                     /clone_lib="Nori Satoh unpublished cDNA library, neural
                     complex"
ORIGIN

  Query Match             78.1%;  Score 16.4;  DB 5;  Length 424;
  Best Local Similarity   94.4%;  Pred. No. 3.7e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGAT 18
              ||||||||| ||||||||
Db        340 TCGTCGAACATTCGAGAT 357


RESULT 14
BI515898
LOCUS       BI515898                439 bp    mRNA    linear   EST 08-APR-2002
DEFINITION  BB160020B20D02.5 Bee Brain Normalized Library, BB16 Apis mellifera
            cDNA clone BB160020B20D02 5', mRNA sequence.
ACCESSION   BI515898
VERSION     BI515898.1  GI:15366272
KEYWORDS    EST.
SOURCE      Apis mellifera (honey bee)
  ORGANISM  Apis mellifera
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
            Apidae; Apis.
REFERENCE   1  (bases 1 to 439)
  AUTHORS   Whitfield,C.W., Band,M.R., Bonaldo,M.F., Kumar,C.G., Liu,L.,
            Pardinas,J., Robertson,H.M., Soares,B. and Robinson,G.E.
  TITLE     Annotated expressed sequence tags and cDNA microarrays for studies
            of brain and behavior in the honey bee
  JOURNAL   Genome Res. 12 (4), 555-566 (2002)
  MEDLINE   21929762
   PUBMED   11932240
COMMENT     Contact: Gene E. Robinson
            Department of Entomology
            University of Illinois
            505 S. Goodwin Ave., Urbana, IL 61801, USA
            Tel: 217 265 0309
            Fax: 217 244 3499
            Email: generobi@life.uiuc.edu
            This research was funded by the University of Illinois Critical
            Research Initiatives Fund and a Burroughs-Wellcome Trust Innovation
            Award in Functional Genomics to G.E. Robinson and an NSF
            Postdoctoral Fellowship in Bioinformatics to C.W. Whitfield.
            PCR PRimers
            FORWARD: TAATACGACTCACTATAGGG
            BACKWARD: ATTAACCCTCACTAAAG
            Plate: BB160020B20  row: D  column: 02
            Seq primer: AGCGGATAACAATTTCACACAGGA
            High quality sequence stop: 439.
FEATURES             Location/Qualifiers
     source          1. .439
                     /organism="Apis mellifera"
                     /mol_type="mRNA"
                     /strain="mixed strains of European bees, predominantly
                     A.m. ligustica"
                     /db_xref="taxon:7460"
                     /clone="BB160020B20D02"
                     /sex="female"
                     /tissue_type="brain"
                     /dev_stage="adult worker honey bee"
                     /lab_host="DH10B"
                     /clone_lib="Bee Brain Normalized Library, BB16"
                     /note="Organ: brain; Vector: pT7T3-Pac; Site_1: EcoR1;
                     Site_2: Not1; The BB16 library was contributed by the
                     Soares laboratory and it was  constructed and normalized
                     as described by Bonaldo, M.F., Lennon, G.  and Soares,
                     M.B. (1996), Genome Research 6(9): 791-806. RNA was
                     prepared from dissected brains of adult worker bees of
                     various ages  and various behavioral groups. "
ORIGIN

  Query Match             78.1%;  Score 16.4;  DB 4;  Length 439;
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```
  Best Local Similarity   94.4%;  Pred. No. 3.7e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 TCGAACGTTCGAGATGAT 21
              |||||||||||| ||||
Db        269 TCGAACGTTCGAGTTGAT 286


RESULT 15
BW300285/c
LOCUS       BW300285                445 bp    mRNA    linear   EST 11-NOV-2002
DEFINITION  BW300285 Nori Satoh unpublished cDNA library, neural complex Ciona
            intestinalis cDNA clone cinc008n07 5', mRNA sequence.
ACCESSION   BW300285
VERSION     BW300285.1  GI:24880896
KEYWORDS    EST.
SOURCE      Ciona intestinalis
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 445)
  AUTHORS   Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
  TITLE     Expressed genes in Ciona intestinalis (2002c)
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .445
                     /organism="Ciona intestinalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:7719"
                     /clone="cinc008n07"
                     /tissue_type="neural complex"
                     /clone_lib="Nori Satoh unpublished cDNA library, neural
                     complex"
ORIGIN

  Query Match             78.1%;  Score 16.4;  DB 5;  Length 445;
  Best Local Similarity   94.4%;  Pred. No. 3.7e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGAT 18
              ||||||||| ||||||||
Db         80 TCGTCGAACATTCGAGAT 63


Search completed: March 30, 2005, 13:25:56
Job time : 3125 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 30, 2005, 10:28:47 ; Search time 501 Seconds
(without alignments)
249.792 Million cell updates/sec

Title: US-10-033-243-132
Perfect score: 21
Sequence: 1 tcgtcgaacgttcgagatgat 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5552208 seqs, 2979665951 residues

Total number of hits satisfying chosen parameters: 11104416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
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17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
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21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	21	100.0	21	14	US-10-033-243-132	Sequence 132, App
2	19	90.5	19	10	US-09-927-422A-16	Sequence 16, Appl
3	19	90.5	19	14	US-10-033-243-19	Sequence 19, Appl
4	19	90.5	19	16	US-10-176-883-41	Sequence 41, Appl
5	19	90.5	19	16	US-10-177-826-41	Sequence 41, Appl
6	19	90.5	19	17	US-10-328-578-41	Sequence 41, Appl
7	19	90.5	19	18	US-10-623-371-41	Sequence 41, Appl
8	19	90.5	19	18	US-10-739-518-41	Sequence 41, Appl
9	19	90.5	22	14	US-10-033-243-30	Sequence 30, Appl
10	19	90.5	22	16	US-10-176-883-52	Sequence 52, Appl
11	19	90.5	22	16	US-10-177-826-52	Sequence 52, Appl
12	19	90.5	22	17	US-10-328-578-52	Sequence 52, Appl
13	19	90.5	22	18	US-10-623-371-52	Sequence 52, Appl
14	19	90.5	22	18	US-10-739-518-52	Sequence 52, Appl
15	18.2	86.7	19	18	US-10-739-518-46	Sequence 46, Appl
16	18	85.7	19	14	US-10-033-243-24	Sequence 24, Appl
17	18	85.7	19	16	US-10-176-883-46	Sequence 46, Appl
18	18	85.7	19	16	US-10-177-826-46	Sequence 46, Appl
19	18	85.7	19	17	US-10-328-578-46	Sequence 46, Appl
20	18	85.7	19	18	US-10-623-371-46	Sequence 46, Appl
21	17.4	82.9	19	14	US-10-033-243-56	Sequence 56, Appl
22	17.4	82.9	19	14	US-10-033-243-57	Sequence 57, Appl
23	17.4	82.9	19	16	US-10-176-883-94	Sequence 94, Appl
24	17.4	82.9	19	16	US-10-176-883-95	Sequence 95, Appl
25	17.4	82.9	19	16	US-10-177-826-94	Sequence 94, Appl
26	17.4	82.9	19	16	US-10-177-826-95	Sequence 95, Appl
27	17.4	82.9	19	17	US-10-328-578-94	Sequence 94, Appl
28	17.4	82.9	19	17	US-10-328-578-95	Sequence 95, Appl
29	17.4	82.9	19	18	US-10-623-371-94	Sequence 94, Appl
30	17.4	82.9	19	18	US-10-623-371-95	Sequence 95, Appl
31	17.4	82.9	19	18	US-10-739-518-45	Sequence 45, Appl
32	17.4	82.9	19	18	US-10-739-518-94	Sequence 94, Appl
33	17.4	82.9	19	18	US-10-739-518-95	Sequence 95, Appl
34	17	81.0	19	14	US-10-033-243-23	Sequence 23, Appl
35	17	81.0	19	16	US-10-176-883-45	Sequence 45, Appl
36	17	81.0	19	16	US-10-177-826-45	Sequence 45, Appl
37	17	81.0	19	17	US-10-328-578-45	Sequence 45, Appl
38	17	81.0	19	18	US-10-623-371-45	Sequence 45, Appl
39	16.4	78.1	18	14	US-10-033-243-14	Sequence 14, Appl
40	16.4	78.1	18	16	US-10-176-883-36	Sequence 36, Appl
41	16.4	78.1	18	16	US-10-177-826-36	Sequence 36, Appl
42	16.4	78.1	18	17	US-10-328-578-36	Sequence 36, Appl
43	16.4	78.1	18	18	US-10-623-371-36	Sequence 36, Appl
44	16.4	78.1	18	18	US-10-739-518-36	Sequence 36, Appl
c 45	16.4	78.1	23	9	US-09-802-686-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-10-033-243-132
; Sequence 132, Application US/10033243
; Publication No. US20030049266A1
; GENERAL INFORMATION:
; APPLICANT: FEARON, Karen L.
; APPLICANT: DINA, Dino
; TITLE OF INVENTION: IMMUNOMODULATORY POLYNUCLEOTIDES AND
; TITLE OF INVENTION: METHODS OF USING THE SAME
; FILE REFERENCE: 377882001800
; CURRENT APPLICATION NUMBER: US/10/033,243
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: 60/258,675
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 132
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-10-033-243-132

Query Match 100.0%; Score 21; DB 14; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGAACGTTCGAGATGAT 21
||||||||||||||||||||
Db 1 TCGTCGAACGTTCGAGATGAT 21

RESULT 2

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US-09-927-422A-16
; Sequence 16, Application US/09927422A
; Publication No. US20030022852A1
; GENERAL INFORMATION:
;  APPLICANT: Van Nest, Gary
;  APPLICANT:  Tuck, Stephen
;  APPLICANT:  Fearon, Karen L.
;  APPLICANT:  Dina, Dino
;  TITLE OF INVENTION: BIODEGRADABLE IMMUNOMODULATORY
;  TITLE OF INVENTION:  FORMULATIONS AND METHODS FOR USE THEREOF
;  FILE REFERENCE: 377882001420
;  CURRENT APPLICATION NUMBER: US/09/927,422A
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: U.S. 09/802,359
;  PRIOR FILING DATE: 2001-03-09
;  PRIOR APPLICATION NUMBER: U.S. 60/188,30
;  PRIOR FILING DATE: 2000-03-10
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Polynucleotide containing CG
US-09-927-422A-16

  Query Match             90.5%;  Score 19;  DB 10;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.6;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATG 19
              |||||||||||||||||||
Db          1 TCGTCGAACGTTCGAGATG 19


RESULT 3
US-10-033-243-19
; Sequence 19, Application US/10033243
; Publication No. US20030049266A1
; GENERAL INFORMATION:
;  APPLICANT: FEARON, Karen L.
;  APPLICANT:  DINA, Dino
;  TITLE OF INVENTION: IMMUNOMODULATORY POLYNUCLEOTIDES AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME
;  FILE REFERENCE: 377882001800
;  CURRENT APPLICATION NUMBER: US/10/033,243
;  CURRENT FILING DATE:  2002-04-03
;  PRIOR APPLICATION NUMBER: 60/258,675
;  PRIOR FILING DATE: 2000-12-27
;  NUMBER OF SEQ ID NOS: 133
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Polynucleotide containing CG
US-10-033-243-19

  Query Match             90.5%;  Score 19;  DB 14;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.6;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATG 19
              |||||||||||||||||||
Db          1 TCGTCGAACGTTCGAGATG 19


RESULT 4
US-10-176-883-41
; Sequence 41, Application US/10176883
; Publication No. US20030175731A1
; GENERAL INFORMATION:
;  APPLICANT: Fearon, Karen
;  APPLICANT:  Dina, Dino
;  APPLICANT:  Tuck, Stephen
;  TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME-I
;  FILE REFERENCE: 377882002000
;  CURRENT APPLICATION NUMBER: US/10/176,883
;  CURRENT FILING DATE:  2002-06-21
;  PRIOR APPLICATION NUMBER: 60/299,883
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: 60/375,253
;  PRIOR FILING DATE: 2002-04-23
;  NUMBER OF SEQ ID NOS: 141
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 41
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-10-176-883-41

  Query Match             90.5%;  Score 19;  DB 16;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.6;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATG 19
              |||||||||||||||||||
Db          1 TCGTCGAACGTTCGAGATG 19


RESULT 5
US-10-177-826-41
; Sequence 41, Application US/10177826
; Publication No. US20030199466A1
; GENERAL INFORMATION:
;  APPLICANT: Fearon, Karen
;  APPLICANT:  Dina, Dino
;  APPLICANT:  Tuck, Stephen
;  TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME-II
;  FILE REFERENCE: 377882002001
;  CURRENT APPLICATION NUMBER: US/10/177,826
;  CURRENT FILING DATE:  2002-06-21
;  PRIOR APPLICATION NUMBER: 60/299,883
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: 60/375,253
;  PRIOR FILING DATE: 2002-04-23
;  NUMBER OF SEQ ID NOS: 141
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 41
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-10-177-826-41

  Query Match             90.5%;  Score 19;  DB 16;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.6;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATG 19
              |||||||||||||||||||
Db          1 TCGTCGAACGTTCGAGATG 19


RESULT 6
US-10-328-578-41
; Sequence 41, Application US/10328578
; Publication No. US20030225016A1
; GENERAL INFORMATION:
```

```
;  APPLICANT: Fearon, Karen L.
;  APPLICANT:  Dina, Dino
;  APPLICANT:  Tuck, Stephen F.
;  TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME-III
;  FILE REFERENCE: 377882002020
;  CURRENT APPLICATION NUMBER: US/10/328,578
;  CURRENT FILING DATE:  2003-05-16
;  PRIOR APPLICATION NUMBER: US 10/176,883
;  PRIOR FILING DATE: 2002-06-21
;  PRIOR APPLICATION NUMBER: US 60/299,883
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: US 60/375,253
;  PRIOR FILING DATE: 2002-04-23
;  PRIOR APPLICATION NUMBER: US 10/177,826
;  PRIOR FILING DATE: 2002-06-21
;  NUMBER OF SEQ ID NOS: 152
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 41
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-10-328-578-41

  Query Match             90.5%;  Score 19;  DB 17;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.6;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATG 19
              |||||||||||||||||||
Db          1 TCGTCGAACGTTCGAGATG 19


RESULT 7
US-10-623-371-41
; Sequence 41, Application US/10623371
; Publication No. US20040132677A1
; GENERAL INFORMATION:
;  APPLICANT: FEARON, Karen L.
;  APPLICANT:  DINA, Dino
;  APPLICANT:  TUCK, Stephen F.
;  TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME-IV
;  FILE REFERENCE: 377882002021
;  CURRENT APPLICATION NUMBER: US/10/623,371
;  CURRENT FILING DATE:  2003-07-18
;  PRIOR APPLICATION NUMBER: US 10/328,578
;  PRIOR FILING DATE: 2002-12-23
;  PRIOR APPLICATION NUMBER: US 10/176,883
;  PRIOR FILING DATE: 2002-06-21
;  PRIOR APPLICATION NUMBER: US 10/177,826
;  PRIOR FILING DATE: 2002-06-21
;  PRIOR APPLICATION NUMBER: US 60/299,883
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: US 60/375,253
;  PRIOR FILING DATE: 2002-04-23
;  NUMBER OF SEQ ID NOS: 158
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 41
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-10-623-371-41

  Query Match             90.5%;  Score 19;  DB 18;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.6;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATG 19
              |||||||||||||||||||
Db          1 TCGTCGAACGTTCGAGATG 19


RESULT 8
US-10-739-518-41
; Sequence 41, Application US/10739518
; Publication No. US20040136948A1
; GENERAL INFORMATION:
;  APPLICANT: Fearon, Karen L.
;  TITLE OF INVENTION: BRANCHED IMMUNOMODULATORY COMPOUNDS AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME
;  FILE REFERENCE: 377882003200
;  CURRENT APPLICATION NUMBER: US/10/739,518
;  CURRENT FILING DATE:  2003-12-17
;  PRIOR APPLICATION NUMBER: US 60/436,406
;  PRIOR FILING DATE: 2002-12-23
;  NUMBER OF SEQ ID NOS: 148
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 41
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-739-518-41

  Query Match             90.5%;  Score 19;  DB 18;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.6;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATG 19
              |||||||||||||||||||
Db          1 TCGTCGAACGTTCGAGATG 19


RESULT 9
US-10-033-243-30
; Sequence 30, Application US/10033243
; Publication No. US20030049266A1
; GENERAL INFORMATION:
;  APPLICANT: FEARON, Karen L.
;  APPLICANT:  DINA, Dino
;  TITLE OF INVENTION: IMMUNOMODULATORY POLYNUCLEOTIDES AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME
;  FILE REFERENCE: 377882001800
;  CURRENT APPLICATION NUMBER: US/10/033,243
;  CURRENT FILING DATE:  2002-04-03
;  PRIOR APPLICATION NUMBER: 60/258,675
;  PRIOR FILING DATE: 2000-12-27
;  NUMBER OF SEQ ID NOS: 133
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Polynucleotide containing CG
US-10-033-243-30

  Query Match             90.5%;  Score 19;  DB 14;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 5.7;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATG 19
              |||||||||||||||||||
Db          4 TCGTCGAACGTTCGAGATG 22


RESULT 10
US-10-176-883-52
; Sequence 52, Application US/10176883
; Publication No. US20030175731A1
```

```
; GENERAL INFORMATION:
;  APPLICANT: Fearon, Karen
;  APPLICANT:  Dina, Dino
;  APPLICANT:  Tuck, Stephen
;  TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME-I
;  FILE REFERENCE: 377882002000
;  CURRENT APPLICATION NUMBER: US/10/176,883
;  CURRENT FILING DATE:  2002-06-21
;  PRIOR APPLICATION NUMBER: 60/299,883
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: 60/375,253
;  PRIOR FILING DATE: 2002-04-23
;  NUMBER OF SEQ ID NOS: 141
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 52
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-10-176-883-52

  Query Match             90.5%;  Score 19;  DB 16;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 5.7;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATG 19
              |||||||||||||||||||
Db          4 TCGTCGAACGTTCGAGATG 22


RESULT 11
US-10-177-826-52
; Sequence 52, Application US/10177826
; Publication No. US20030199466A1
; GENERAL INFORMATION:
;  APPLICANT: Fearon, Karen
;  APPLICANT:  Dina, Dino
;  APPLICANT:  Tuck, Stephen
;  TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME-II
;  FILE REFERENCE: 377882002001
;  CURRENT APPLICATION NUMBER: US/10/177,826
;  CURRENT FILING DATE:  2002-06-21
;  PRIOR APPLICATION NUMBER: 60/299,883
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: 60/375,253
;  PRIOR FILING DATE: 2002-04-23
;  NUMBER OF SEQ ID NOS: 141
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 52
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-10-177-826-52

  Query Match             90.5%;  Score 19;  DB 16;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 5.7;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATG 19
              |||||||||||||||||||
Db          4 TCGTCGAACGTTCGAGATG 22


RESULT 12
US-10-328-578-52
; Sequence 52, Application US/10328578
; Publication No. US20030225016A1
; GENERAL INFORMATION:
;  APPLICANT: Fearon, Karen L.
;  APPLICANT:  Dina, Dino
;  APPLICANT:  Tuck, Stephen F.
;  TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME-III
;  FILE REFERENCE: 377882002020
;  CURRENT APPLICATION NUMBER: US/10/328,578
;  CURRENT FILING DATE:  2003-05-16
;  PRIOR APPLICATION NUMBER: US 10/176,883
;  PRIOR FILING DATE: 2002-06-21
;  PRIOR APPLICATION NUMBER: US 60/299,883
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: US 60/375,253
;  PRIOR FILING DATE: 2002-04-23
;  PRIOR APPLICATION NUMBER: US 10/177,826
;  PRIOR FILING DATE: 2002-06-21
;  NUMBER OF SEQ ID NOS: 152
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 52
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-10-328-578-52

  Query Match             90.5%;  Score 19;  DB 17;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 5.7;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATG 19
              |||||||||||||||||||
Db          4 TCGTCGAACGTTCGAGATG 22


RESULT 13
US-10-623-371-52
; Sequence 52, Application US/10623371
; Publication No. US20040132677A1
; GENERAL INFORMATION:
;  APPLICANT: FEARON, Karen L.
;  APPLICANT:  DINA, Dino
;  APPLICANT:  TUCK, Stephen F.
;  TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME-IV
;  FILE REFERENCE: 377882002021
;  CURRENT APPLICATION NUMBER: US/10/623,371
;  CURRENT FILING DATE:  2003-07-18
;  PRIOR APPLICATION NUMBER: US 10/328,578
;  PRIOR FILING DATE: 2002-12-23
;  PRIOR APPLICATION NUMBER: US 10/176,883
;  PRIOR FILING DATE: 2002-06-21
;  PRIOR APPLICATION NUMBER: US 10/177,826
;  PRIOR FILING DATE: 2002-06-21
;  PRIOR APPLICATION NUMBER: US 60/299,883
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: US 60/375,253
;  PRIOR FILING DATE: 2002-04-23
;  NUMBER OF SEQ ID NOS: 158
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 52
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-10-623-371-52

  Query Match             90.5%;  Score 19;  DB 18;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 5.7;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATG 19
```

```
                  ||||||||||||||||||
Db          4 TCGTCGAACGTTCGAGATG 22


RESULT 14
US-10-739-518-52
; Sequence 52, Application US/10739518
; Publication No. US20040136948A1
; GENERAL INFORMATION:
;  APPLICANT: Fearon, Karen L.
;  TITLE OF INVENTION: BRANCHED IMMUNOMODULATORY COMPOUNDS AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME
;  FILE REFERENCE: 377882003200
;  CURRENT APPLICATION NUMBER: US/10/739,518
;  CURRENT FILING DATE:  2003-12-17
;  PRIOR APPLICATION NUMBER: US 60/436,406
;  PRIOR FILING DATE: 2002-12-23
;  NUMBER OF SEQ ID NOS: 148
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 52
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-739-518-52

  Query Match             90.5%;  Score 19;  DB 18;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 5.7;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATG 19
              |||||||||||||||||||
Db          4 TCGTCGAACGTTCGAGATG 22


RESULT 15
US-10-739-518-46
; Sequence 46, Application US/10739518
; Publication No. US20040136948A1
; GENERAL INFORMATION:
;  APPLICANT: Fearon, Karen L.
;  TITLE OF INVENTION: BRANCHED IMMUNOMODULATORY COMPOUNDS AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME
;  FILE REFERENCE: 377882003200
;  CURRENT APPLICATION NUMBER: US/10/739,518
;  CURRENT FILING DATE:  2003-12-17
;  PRIOR APPLICATION NUMBER: US 60/436,406
;  PRIOR FILING DATE: 2002-12-23
;  NUMBER OF SEQ ID NOS: 148
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 46
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 5
;   OTHER INFORMATION: b is 5-bromocytosine
US-10-739-518-46

  Query Match             86.7%;  Score 18.2;  DB 18;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 15;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATG 19
              ||||:||||||||||||||
Db          1 TCGTBGAACGTTCGAGATG 19


Search completed: March 30, 2005, 12:33:39

Job time : 502 secs
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